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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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4	g in E	1250 Norris k, H.; an, J.;		s, S.J.; Richard: ; Smith,	8	Weins Ison, I	<pre>sstock, G.M.; White, O.; Su D.; Howell, J.K.; Chidamba .; Venter, J.C.</pre>	ttton, G.G.; Dodson, R.; iram, M.; Utterback, T.;
4	Complete Ce number	te g ber:	, p (4	250 250	equen;	ე. D.:	ce of Treponema pallidum, the 0:98332770	syphilis spirochete.
A; Status: preliminar A; Molecule type: DNA A; Residues: 1-956 <cc A; Cross-references: 0</cc 	is: preliminary ule type: DNA ues: 1-956 <co:< td=""><td>minar DNA 56 &lt;0</td><td>&gt; 6.3</td><td>nuc AE0</td><td>ic 27</td><td>, a</td><td>acid sequence not shown; tran: ; GB:AE000520; NID:g3323363;</td><td>Islation not shown PIDN:AAC26589.1; PID:933</td></co:<>	minar DNA 56 <0	> 6.3	nuc AE0	ic 27	, a	acid sequence not shown; tran: ; GB:AE000520; NID:g3323363;	Islation not shown PIDN:AAC26589.1; PID:933
C; Genetics A; Genetics C; Superfam	035	ya]	9 9-	-tRNA	= = ;	. 6.4		
Query Mar	tch	٠ .			8.	ر مور ال	Score 48; DB 2; Length	nues 56;
Best Loc Matches Qy 3	AL SI B; AWOLA AWOKA	MILAR COD: KOKAU: -11	Larity Conser KAQEAE	y 5 rvati EK 16  : ER 90	/ . I ve 5	·.	Pred. No. 14; 3; Mismatches 3; Indel	s 0; Gaps 0;
RESULT 2								
ng ag i	ase Clp e names adenos	Clp A mes: enosi		binding characteristic characteristi	ng (	2 3	ain B - Rickettsia prowazek .Clp proteinase regulatory .ase (EC 3.6.1.3)	di chain
200	: Rickettsia  -Nov-1998 # on: D71711	1998 1711	# 50 6	sequence_re	ICe_	. > 3	vision 21-Nov-1998 #text_c	e 19-Jan-2001
ກິດ	The genome	-140 nome ber:	1 H 0 L	38 1en 530		4	Rickettsia prowazekii and 0:99039499	the origin of mitochondria
A; Accession A; Status: A; Molecule	_ 0	7.50	ry; A	nucl	eic	ď	acid sequence not shown; trans	slation not shown
A; Cross-re A; Experime C; Genetics	feren feren ntal	ູຂອ	O 00 ··	Str	3527( ain M	O; O Madı	GB:AJ235269; NID:93860572; drid E	PIDN:CAA14507.1; PID:938

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Cidencesion: E71414

Ribevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D. P.; Wedler, H.; Wedler, H.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; C. avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeifer, M.; Funk, H. Nature 391, 485, 488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N. A; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; A; Fitter analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis the A; Accession: E71414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Kluyvera cryocrescens
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A25528
R.Barbero, J.L.: Buesa, J.M.; Gonzalez de Buitrago, G.; Mendez, E.; Perez-Aranda, A.:
Gene 49, 69-80, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete nucleotide sequence of the penicillin acylase gene from Kluyvera ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-736 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: (33-Aug-1998 *sequence_revision 03-Aug-1998 *text_change 05-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:297337; NID:92244829; PID:e327432; PID:92244865
C:Genetics:
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C;Superfamily: penicillin amidase
C:Keywords: antiblotic resistance; hydrolase; penicillin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: the authors translated the codon CAG for residue 719 as Glu A;Note: the source is designated as Kluyvera citrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: penicillin acylase; penicillin amidohydrolase
                                                                                                                                                                                                              Ouery Match 51.8%; Score 43; DB 2; Length 685; Best Local Similarity 63.6%; Pred. No. 63; Astches 7; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.6%; Score 42; DB 2; Length 736;
53.3%; Pred. No. 98;
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                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                       A;Gene: metG; NNAO275
C;Superfamily: methionine--tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M15418
A;Experimental source: ATCC 21285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Salmonella enterica subsp. enterica serovar Typhi (strain Species: Salmonella enterica serovar Typhi (strain Species: Salmonella enterica subsp. enterica serovar Typhi Note: this species has also been called Salmonella typhi Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Accession: AB0514 Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Litter 413, 848-852, 2001
Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
                                                          Description: allows clpP to hydrolyze polypeptides and proteins, probably by a chaperd activity; ATP hydrolysis is required for Clp hydrolysis of proteins but not of smaller Superfamily: endopeptidase Clp ATP-binding chain chaperone; ATP; hydrolase; molecular chaperone; nucleotide binding; P-loop 207-214/Region: nucleotide-binding motif A (P-loop) 257-260/Region: nucleotide-binding motif B (04-611/Region: nucleotide-binding motif B (67-677/Region: nucleotide-binding motif B (7-loop)
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Molecula type: DNA
Residues: 1-685 <PAR>
Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83583.1; PID:g737903
Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ithionine--tRNA ligase (EC 6.1.1.10) NMA0275 [imported] - Neisseria meningitidis (strai
Species: Neisseria meningitidis
Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, ture 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.4%; Score 46; DB 2; Length 858; 47.1%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                               213/Binding site: ATP (Lys) #status predicted 610/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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Superfamily: dnaJ amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 NTKWOAEKSKLOOAOKL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 47.1 Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QLAKQKAQEAEK 16
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Residues: 1-270 <PAR>
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Gene: clpB; RP036
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Gaps

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ATILIE: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300, MUID:98196666
A,Racession: D70437
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Rolecule type: DNA
A,Residues: 1-185 cAQFA
A,Cross-references: GB:AE000746; NID:92983925, PIDN:AAC07478.1; PID:92983929; GB:AE0
A,Experimental source: strain VF5
A,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Erwina cartorogra

Cispecies: Mittombe, D.; Wharam, S.; Gibson, M.; Allison, G.; Bunce, N.; Baral

Mol. Microbiol. 8, 443-456, 1993

Mol. Microbiol. 8, 443-456, 1993

A; Reference number: S32857; MUID:93316842

A; Reference number: S32857; MUID:93316842

A; Status: preliminary: nucleic acid sequence not shown; translation not shown

A; Status: preliminary: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-188 KREE>

A; Cross-references: EMBL:X70049; NID:942184; PIDN:CAA49649.1; PID:942190

C; Genetics:
                         A;Description: hydrolyzes penicillins G and V into fatty acid and 6-aminopenicillani C;Superfamily: penicillin amidase
C;Keywords: antibiotic resistance; hydrolase; penicillin resistance
F;1-26/Domain: signal sequence *status predicted <SIG>
F;27-846/Product: penicillin amidase zynogen *status predicted <PRO>
F;290-846/Product: penicillin amidase heavy chain *status predicted <MPT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
V.
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C;Species: Aquifex aeolicus
C;Bate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70437
                                                                                                                                                                                                                                                                                                                                           Gaps
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41.2%; Pred. No. 1.1e+02;
Live 5; Mismatches 5; Indels
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81.8%; Pred. No. 35;
tive 1; Mismatches
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49.4%; Score 41; DB 2;
Best Local Similarity 72.7%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     1 SSAWQLAKQKAQEAEKL 17
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Matches 7; Conservative
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;Reference number: 154005; MUID:87219870
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:Residues: 1-67, R',69-76, R',78-96, S',98-129, T',131-216, G',218-341,'L',343,'WF',376
:Cross-references: GB:M11672; NID:g147044; PIDN:AAA24258.1; PID:g147047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein
Residues: 27.36.291-299 <5LA>
Bruns, W.: Hoppe, J.; Tsai, H.; Bruening, H.J.; Maywald, F.; Collins, J.; Mayer, H.
Mol. Appl. Genet. 3, 36-44, 1965
Title: Structure of the penicillin acylase gene from Escherichia coli: A periplasmic
Reference number: 156367; MulD:85236066
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                                                                                                                                                                                                                                                                                                                                                                                                            Species: Escherichia coli

:Species: Escherichia coli

:Date: 30-Sep-1987 #sequence_revision 26-Jan-1996 #text_change 18-Jun-1999

:Schumacher, G.; Sizmann, D.; Haug, H.; Buckel, P.; Bock, A.

ucleic Acids Res. 14, 5713-5727, 1986

:Title: Penicillin acylase from E. coli: unique gene-protein relation.

:Reference number: A23593; MUID:86286584
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Residues: 741-788, °Q',790-846 <RE3>
:Cross-references: GB:Ml2373; NID:9147045; PIDN:AAA24259.1; PID:9147048
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                                                                                                                                                                                                                                                                                                                                                                  enicillin amidase (EC 3.5.1.11) precursor - Escherichia coli
Alternate names: penicillin G acylase; penicillin G amidohydrolase
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                      50.6%; Score 42; DB 1; Length 844; 41.2%; Pred. No. 1.1e+02; tive 5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Reference number: S23375; MUID:88056318;Accession: S23375
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                                                                                                                                                                                         |: | : | || : | 290 SNMWVIGKNKAQDAKAI 306
Ouery Match
Best Local Similarity 41.22
Best Local 7; Conservative
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Residues: 1-846 <SCH>
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2091-2098, 2001
Science 293, 2098-2001
A;Tille: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Cross-references: EMBL:274079; NID:91431009; PIDN:CAA98590.1; PID:e252986; PID:9143
A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000019; PIDN:BAB73355.1; PID:g17130745; GSPUH:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE006914; PIDN: AAL02597.1; PID: q15619095; GSPUB: GN00173
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S6756
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clpB protein (imported) • Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
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C:Keywords: ATP: nucleotide binding; P-loop
F:181-188/FRegion: nucleotide-binding motif A (P-loop)
F:284-289/Region: nucleotide-binding motif B
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C:Superfamily: endopeptidase Clp ATP-binding chain
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AWULAKOKAUEA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-844 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-857 <KUR>
                                                                                                                                                                                                   A;Status: preliminary
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                                                                                                                                                         A; Accession: AC1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C97707
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A; Molecule type: DN
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                                                                                                                                                                                                                obable receptor/regulator protein STV2545 [imported] - Salmonella enterica subsp. ente Species: Salmonella enterica subsp. enterica serovar Typhi Note: this species has also been called Salmonella typhi Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Accession: A10795
                                                                                                                                                                                                                                                                                                                                                                              Parkhill, J.; Bougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov Reference number: A80502; PMJD:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Anabaena Sp. (Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 Accession: AC1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
Accession: T46922
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Species: Anabaena sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S. bmitted to the Protein Sequence Database, February 2000
Reference number: 224138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 49.4%; Score 41; DB 2; Length 334; Best Local Similarity 61.5%; Pred. No. 64; Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 41; DB 2; Length 409; 50.0%; Pred. No. 78;
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Best Local Similarity
Matches 8; Conservai
   2 SAWQLAKQKAQ 12
                                                                 42 SAWQLARFQAQ 52
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Molecule type: DNA
Residues: 1-334 <PAR>
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Molecule type: mRNA
Residues: 1-409 <AAA>
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Note: DKF2p434B1612.1
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0; Gaps
                                                                                     Length 995;
                                                                                  Ouery Match 49.4%; Score 41; DB 2; Length 995; Best Local Similarity 69.2%; Pred. No. 1.9e+02; Matches 9; Conservative 2; Mismatches 2; Indels
;288-291/Region: DEAD motif
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5 QLAKQKAQEAHKL 17

|||||: | :|||| | 621 QLAKKTAMKAEKL 633 Ω

ranscription-repair coupling protein MId PA3002 [imported] - Pseudomonas aeruginosa (st :Species: Pseudomonas aeruginosa :Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

Accession: D83270
Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br dman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lorry, S.; Olson, M.V.
alure 406, 959-964, 2000
;Title Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor Reference number: A82950; MUID:20437337

Status: preliminary :Molecule type: DNA :Residues: 1-1148 <STG> :Cross-references: GB:AE004725; GB:AE004091; NID:99949100; PIDN:AAG06390.1; GSPDB:GN001 :Experimental source: strain PAO1

;Superfamily: transcription-repair coupling protein ;Gene: mfd; PA3002

0; Gaps Query Match 49.4%; Score 41; DB 2; Length 1148; Best Local Similarity 61.5%; Pred. No. 2.2e+02; Matches 8; Conservative 1; Mismatches 4; Indels

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1 SSAWQLAKQKAQE 13

earch completed: August 6, 2002, 17:05:15 ob time: 917 sec

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083998 treponema p
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                                                                                        August 6, 2002, 17:07:34 ; Search time 32.88 Seconds
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P76481
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                105224 seqs, 38719550 residues
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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042131 gallus gall	TP2B_CHICK	_	1627	45.8	38	45
Q02880 homo sapie	TP2B_HUMAN		1626	45.8	38	44
Q64511 mus muscul	TP2B_MOUSE	П	1612	45.8	38	43
Q64399 cricetulus	TP2B_CRILO	-	1612	45.8	38	42
P09790 neisseria	IGA_NEIGO	7	1532	45.8	38	41
09vfb7 drosophila	Y623_DROME	٦	1145	45.8	38	40
004932 craterost	SPS1_CRAPL	-4	1054	45.8	38	39
Q9yfzl aeropyrum	RASO_AERPE	,-	919	45.8	38	38
P57972 pasteurel	MUTS_PASMU	_	860	45.8	38	37
P57838 pasteurel	SYM_PASMU	Н	682	45.8	38	36
P43828 haemophilus	SYM_HAEIN	-	682	45.8	38	35
P09883 escherichia	CEA9_ECOLI	-	582	45.8	38	34

## ALIGNMENTS

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                                                                                                                                                                                                                                                 STRAINNICHOLS;
MEDLINE-98312770; PubMed-9665876;
Fraser C.M., Onris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujil C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) - AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + L-valyl-trna(val).
-:- SUBUNT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                      15-DEC-1998 (kel. 37, Last sequence update)
16-CCT-2001 (kel. 40, Last annotation update)
Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
VALS OR TP1035.
                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "KMSKS" REGION.
ATP (BY SIMILARITY).
1; 7D50583C7C6BA35A CRC64;
                                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                  956 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00178; AA_TRNA_LIGASE_I; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interpro; IPR002300; tRNA-synt_la.
Interpro; IPR001412; tRNA-synt_l.
Interpro; IPR002303; tRNA-synt_val.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107362 MW;
                                                                     15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001271; AAC26589.1; -.
HSSP; P96142; 1GAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00133; tRNA-synt_1; 1
PRINTS; PR00986; TRNASYNTHVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 281:375-388(1998).
                                    STANDARD;
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570
569
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=160;
                                  SYV_TREPA
083998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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RESULT 1
SYV_TREPA
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SUBCELLLAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY $45 (SERINE PHOTFASE) ALSO
KNOWN AS THE PENICILLIN ACYLASE FAMILY.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92109664; PubMed=1764029;
Martin J., Slade A., Altken A., Arche R., Virden R.;
"Chemical modification of serine at the active site of penicillin acylase from Kluyvera citrophila.";
Biochem. J. 280:659-662[1931].
-!- CATALYTIC ACTIVITY: Penicillin + H(2)0 = a fatLy acid anion + 6-
                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbero J.L., Buesa J.M., de Buitrago G.G., Mendez E., Perez-Aranda A., Carcia J.L., "Complete nucleotide sequence of the penicillin acylase gene from Kluyvera citrophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kluyvera citrophila (Kluyvera cryocrescens).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENICILLIN G ACYLASE ZYMOGEN.
PENICILLIN G ACYLASE ALPHA SUBUNIT.
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Pfam; PF01804; Penicil_amidase; 1.
Hydrolase; Antibiotic resistance: 2ymogen; Periplasmic; Signal.
SIGNAL 1 26
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57.8%; Score 48; DB 1; Length 956; 57.1%; Pred. No. 6.2; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3466059B0FC4E5AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 21285,
MEDLINE=87192002; PubMed-3032748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 290-297, AND ACTIVE SITE.
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                                                                Conservative
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HSSP; P06875; 1AJQ.
                           Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 49:69-80(1986)
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290
290
844 AA;
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   Query Match
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Score 42; DB 1; Length 844; Pred. No. 47;

Query Match Best Local Similarity

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Gaps
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16-OCT-2001 (Rel. 40, Last annotation update)
Penicilin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ob S.-J., Kim Y.-C., Park Y.-W., Min S.-Y., Kim I.-S., Kang H.-S., "Complete nucleotide sequence of the pericillin G acylase gene and the flanking regions, and its expression in Escherichia coli."; Gene 56:87-97 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87219870; PubMed-3556321; Malle F., Gosset G., Tenorio B., Oliver G., Bolivar F.; "Characterization of the regulatory region of the Escherichia coli penicillin acytase structural gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A common precursor for the two subunits of the penicillin acylase from Escherichia coli ATCC11105.";
                                                                                                                                                                                                                                                                                                                                                                                              Schumacher G., Sizmann D., Haug H., Buckel P., Boeck A.; "Penicillin acylase from E. coll: unique gene-protein relation."; Nucleic Acids Res. 14:5713-5727(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AFCC 11105;
MEDILINE-66137424; PubMed+3005131;
Oliver G., Valle F., Rosettí F., Gomez-Pedrozo M., Santamaria P.,
Gosset G., Bolivar F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transcriptional and gene fusion analyses of the Escherichia coli
                                                                                                                                                                                                                                                                                                 Bacteria; Proleobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Penicillin acylase has a single-amino-acid catalytic centre.";
Nature 373:264-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 11105;
MEDLINE-95115804; Pubmed-7816145;
Duggleby_H.J., Tolley S.P., Hill C.P., Dodson E.J., Dodson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sizmann D., Keilmann C., Boeck A., "Primary structure requirements for the maturation in vivo of penicillin acylase from Escherichia coli ATCC 11105.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radoja S., Francetic O., Stojicevic N., Moric I., Glisin S.,
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               penicillin amidase gene expression.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
٠,
                                                                                                                                                  846 AA.
   Mismatches
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                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-88056318; PubMed-3315861;
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5
                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                               (Penicillin G amidohydrolase).
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                                                    290 SNMWVIGKNKAQDAKAI 306
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                               1 SSAWQLAKQKAQEAEKL 17
7; Conservative
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 50:119-122(1986).
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                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                           PAC_ECOL1
P06875;
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Matches
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                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                          -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A BETA CHAIN.
-!- SUBCELLIOUR LOCATION: PETIDIASMIC.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S45 (SERINE PROTEASE) ALSO
KNOWN AS THE PENICILLIN ACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
CATALYTIC ACTIVITY: Penicillin + H(2)0 = a fatty acid anion + 6-
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PENICILLIN G ACYLASE ALPHA SUBUNIT.
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Hydrolase; Antibiotic resistance; Zymogen; Periplasmic; Signal;
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16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)
(Transcriptase omega chain) (RNA polymerase omega subunit).
RPOZ OR SPY1630.
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A -> R (IN REF. 3).
I -> T (IN REF. 3).
R -> P (IN REF. 3).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
G -> P (IN REF. 2).
G -> P (IN REF. 2).
W; 48570EDC853BA227 CRC64;
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                 aminopenicillanate
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1103
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1AJP;
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P82577;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, I BETA' CHAIN AND I OMEGA CHAIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE RNA POLYMERASE OMEGA CHAIN FAMILY.
                                                                                                                     Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clitton S.W., Roe B.A., McLaughlin R.Kreptococcus pyogenes."; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reeves P.J., Whitcombe D., Wharam S., Gibson M., Allison G., Bunce N., Barallon R., Douglas P., Mulholland V., Stevens S., Walker S.,
                                                                                                                                                                                                                                                                                                          Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J., VanBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                  -I-FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-terminal regions of the beta 'subunit thereby facilitating its interaction with the beta and alpha subunits (By similarity)-I-CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                      'Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
General secretion pathway protein H precursor (Pectic enzymes secretion protein outH).
                                                                                                                                                                                                                                                                       SEQUENCE OF 27-42; 46-60 AND 97-104, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 41; DB 1; Length 104; 53.8%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 AA; 11705 MW; FD6FDF3D852CC7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                             STRAIN-SF370 / AICC 700294 / Serotype MI; MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93316842; PubMed=8326859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE006594; AAK34401.1; -.
                                                                                                                                                                                                                                                                                      STRAIN-JRS4 / Serotype M6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 53...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 QIAKEKEEEGEKI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ULAKOKAQEAEKI, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                        NCB1_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                               proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSPH_ERWCA
P31587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPH_ERWCA
a
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SO THE FEW SO DESCRIPTION OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license effectment (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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               "Molecular cloning and characterization of 13 out genes from Erwinia carotovora subspecies carotovora: genes encoding members of a general secretion pathway (GSP) widespread in Gram-negative bacteria."; Mol. Microbiol. 8:443-456(1993).

-i- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burger F., Daugeron M.-C., Linder P.;
"Deplop, a putative RNA helicase from Saccharomyces cerevisiae, is required for ribosome biogenesis.";
Nucleic Acids Res. 28:2315-2323(2000).
-!- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE. PROBABLY INTERACTS WITH 60S RIBOSOMAL SUBUNIT. INVOLVED IN THE MATURATION OF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL SECRETION PATHWAY PROTEIN H. METHYLATION (BY SIMILARITY)
733E90BFDDD6C5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! . SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-! - SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. HIGHLY SIMILAR TO S.POMBE SPAC31A2.07C.
                                                                                                                                                                                                 MULTIPLE PECTIC ENZYMES.
-:- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable RNA-dependent helicase DBP10 (DEAD-box protein 10).
DBP10 OR YDL031W OR D2770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.4%; Score 41; DB 1; Length 188; 72.7%; Pred. No. 16; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paulin L., Saren A.M.;
Submitted (APR-1996) to the EMBL/GenBank/NUBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO01120; Prok_N_methyltn.
PRINTS; PR00885; BCTERIALGSPH.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE-20330350; PubMed-10871363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S31751; S31751.
PIR; S32862; S32862.
InterPro: JPR002416; Bac_GSPH.
InterPro: JPR001120: Prok_N_me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 188 AA; 21390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X70049; CAA49649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 72.7% les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SAWQLAKQKAQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
Salmond G.P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C
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MEDLINE-94150718: PuthMed-7906498;
WISSON K., Adiscough K., Anderson K., Baynes C., Berks M.,
Wilson K., Ainscough K., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Garder A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster A.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2 Mb of contiguous nucleotide sequence from chromosome 111 of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

49.4%; Score 41; DB 1; Length 995;
Best Local Similarity 69.2%; Pred. No. 78;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 134.9 kDa proțein ZK512.5 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      995 AA; 113157 MW; 9AFA74D0BAB198A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; RNA-binding; Helicase; Nuclear protein. NP_BIND 181 188 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                   DEAD_ATP_helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEAD BOX.
                                                                                                                                                                                                                                              EMBL, Z74079; CAA98590.1; -. SGD: S0002189; DBP10. InterPro; IPR001410; DEAD. InterPro; IPR000629; DEAD.ATP_he InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00270; DEAD; 1.
Pfam; PF00271; heLicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                       EMBL; 271781; CAA96458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    621 QLAKKTAMKAEKL 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 QLAKQKAQEAEKL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOQ5_CAEEL
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4 WQI,AKQKAQEAE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                341 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                Q06486; 1CKI.
                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                            NCBI_TaxID-6239;
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SEQUENCE
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                 Score 41; DB 1; Length 1232;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.2%; Score 40; DB 1; Length 190; Best Local Similarity 66.7%; Pred. No. 23; Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                                    2; Indels
                                                  1232 AA; 134923 MW; 6DFC35D664AA8D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL,
A810954296FBE099 CRC64;
                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                    01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Septum formation protein Maf.
                                                                                                                                                                                                  190 AA.
                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                      STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP001517; BAB06752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE 33 33 SS PASEQUENCE 190 AA; 21240 MW;
                                                                                 49.48;
          EMBL; Z22177; CAA80146.1; -.
                   PIR, S40766; S40766.
WormPep; ZK512.5; CE00411.
Hypothetical protein.
SEQUENCE 1232 AA; 13492
                                                                       Ouery Match
Best Local Similarity 53.3.
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003697; Maf.
Pfam; PF02545; Maf; 1.
                                                                                                                                              326 AYEKARQEAAESEKL 340
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                           3 AWOLAKOKAQEAEKL 17
                                                                                                                                                                                                                                                                          Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 QLARQKAQDVAK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID #86665;
                                                                                                                                                                                                                                                                OR BH3033
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ID YKL1_CAEEL
                                                                                                                                                                                                   MAF_BACHD
                                                                                                                                                                                        MAF_BACHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS500111; PROTEIN_KINASE_DOM; 1.
Hypothetical protein; Transferase; Serine/threonine-protein kinase; APP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C-125 / JCM 9153;
MEDLINE-20512582: PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative casein kinase 1 C03C10.1 in chromosome III (EC 2.7.1.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
17AD6E173551BABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY). ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                     Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39037 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; C03C10.1; CE00872.
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45
135
                                                                                                                                                                    Caenorhabditis elegans.
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Bacillus halodurans.
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VARIANT DFNA22 TYR-442.
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sec http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avraham K.B., Hasson T., Sobe T., Balsara B., Testa J.R., Skvorak A.B., Morton C.C., Copeland N.G., Jenkins N.A.; "Characterization of unconventional MYO6, the human homologue of the responsible for deafness in Snell's waltzer mice."; Hum. Mol. Genet. 6:1225-1231(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
            "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wells A.L., Lin A.W., Chen L.-Q., Safer D., Cain S.M., Hasson T., Carragher B.O., Milligan R.A., Sweeney H.L.; "Myosin VI is an actin-based motor that moves backwards."; Nature 401:505-508(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMARI; SWOOD43; SMR; 1.
PROSITE; PSO0486; DNA_MISMATCH_REPAIR_2; FALSE_NEG.
ATP-binding; DNA-binding; Complete proteome.
NP_BIND 335 342 ATP (POTENTIAL).
NP_BIND 705 AA 87426 MW; DBED779F2F4671C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99447046; PubMed=10519557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97402203; PubMed=9259267;
                                                                                                                                                                                                                                                                                                                                          EMBL; AP001517; BAB06825.1; -.
InterPro: IPR000432; MutS.C.
InterPro: IPR002683; MutS.N.
InterPro: IPR002683; Smr.
Pfam: PF00488; MutS.C: 1.
Pfam: PF01713; Smr: 1.
ProDom: PD001263; MutS.C: 1.
SMART; SM00534; MUTS.C: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 8; Conserva
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  Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avraham K.B.;
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Q9UM54;
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                                                                                                                                                                                                                                                                   -i- FUNCTION: RECESSIVE ACTIN-BASED MOTOR. REQUIRED FOR STRUCTURAL INTEGRATY OF INNER EAR HAIR CELLS (BY SIMILARITY).

-i- DISEASE: Defects in MYOG are the cause of an autosomal dominant form of nonsyndromic sensorineural deafness (DFNA22). The deafness is progressive and postlingual, with onset during childhood (8 to 10 years of age at onset of symptoms; 6 to 8 years of age at onset of first audiometric abnormalities). By the age of approximately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
MEDLINE-21375673; PubMed-11468689; Melchionda S., Ahituv N., Bisceglia L., Sobe T., Glaser F., Rabionet R., Arbones M.L., Notarangelo A., Di Iorio E., Carella M., Zelante L., Estivill X., Avraham K.B., Gasparini P.; "MYO6, the human homologue of the gene responsible for deafness in Snell's waltzer mice, is mutated in autosomal dominant nonsyndromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 years, affected individuals invariably have profound sensorineural deafness.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.2%; Score 40; DB 1; Length 1262; 56.2%; Pred. No. 1.4e+02;
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1262 AA; 146047 MW; CFIFA35796FC1C60 CRC64;
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Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Disease mutation; Deafness.
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ACTIN-BINDING (POTENTIAL).
C -> Y (IN DFNA22).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.4e-3; Mismatches
                                                                                                                                                                                                                                       Genet. 69:635-640(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF00063; myosin_head; 1.
PRINTS: PR0193; MYOSINHEAVY.
PRODom: PD000035; myosin_head; 1.
SMART: SM00015; IQ; 1.
SMART: SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001609; IQ.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                               hearing loss.
                                                                                                                                                                                                                                           Hum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                      TISSUE-Brain;
BDLINE-96083582; PubMed-7493015;
Avraham K.B., Hasson T., Steel K.P., Kingsley D.M., Russell L.B.,
Mooseker M.S., Copeland N.G., Jenkins N.A.;
The mouses Snell's waltzer deafness gene encodes an unconventional
myosin required for structural integrity of inner ear hair cells.";
Nat. Genet. 11:369-375[1955].
                                                                                                                                                                                                                                                                                                     CONDITION CHARACTERIZED BY CIRCLING, HEAD-TOSSING, DEAFNESS AND
                                                                                                                                                                                                           INTEGRITY OF INNER EATHN BASED MOTOR. REQUIRED FOR STRUCTURAL INTEGRITY OF INNER EAR HAIR CELLS (BY SIMILARITY).

1. TISSUE SPECIFICITY: WIDELY EXPRESSED. WITHIN THE COCHLEA, EXPRESSED SPECIFICALLY WITHIN THE SENSOR HAIR CELLS.

1. DISEASE: DEFECTS IN MYOG ARE THE CAUSE OF SNELL'S WALTZER, A
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
General secretion pathway protein H precursor (Pectic enzymes secretion protein outH).
                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.2%; Score 40; DB 1; Length 1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN SNELL'S WALTZER).
W; 4F51ABC72463148C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.4e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; FALSE_NEG.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation; Deafness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40D; MGI:104785; Myo6.
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SMO0015; IQ; 1.
SMART; SMO0242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146408 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U49739; AAB00194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia chrysanthemi.
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668
766
1265
1265 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00612; IQ;
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                                                                                                                                                                                                                                                                                                                          HYPERACTIVITY
                                NCB1_Tax1D-10090;
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P24687;
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DOMAIN
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ID GSPH_ER
PT 01-MAR
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DE GENETA
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                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi: sequence comparison with secretion genes from other Gram-negative bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  He S.Y., Lindeberg M., Chatterjee A.K., Collmer A., "Cloned Erwinia chrysanthemi out genes enable Escherichia coli to selectively secrete a diverse family of heterologous proteins to its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 88:1079-1083(1991).
-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL SECRETION PATHWAY PROTEIN H. METHYLATION (BY SIMILARITY). 7E72A931042B63B8 CRC64;
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
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InterPro; IPR001120; Pro_N_methyltn.
PRIMTS; PR00865; BCTERIALGSPH.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol, 174:7385-7397(1992).
                                                                                                                                                                                                                                                                                        MEDLINE-93054355; PubMed-1429461;
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MEDLINE=91012805; PubMed=2214027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91126059; PubMed-1992458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES 6 6 M
SEQUENCE 181 AA; 20288 MW;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                       Lindeberg M., Collmer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                SEQUENCE FROM N.A
                                         Pectobacterium.
                                                                                        NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-EC16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AANT_HDVS1
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     SPHHES SPECIOL COCCOCCOCC SPHES SPECIAL SPECIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SMISs Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      SEQUENCE FROM N.A.
STRAIM-ISOLARE 7/18/83;
STRAIM-ISOLARE 7/18/83;
IMAZEKI F., OMATA M., Obto M.;
Imazeki F., Omata M., Obto M.;
"Complete nucleotide sequence of hepatitis delta virus kNA in Japan.";
Nucleic Acids Res. 15:5439-5439(1991).
                                                                                                                                                                                                                                                                        -1- DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC HEPATITIS DELTA VIRAL INFECTIONS.
-1- MISCELLANEOUS: DELTA ANTIGEN BINDS SPECIFICALLY TO HDV KNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Imazeki F., Omata M., Ohto M.;
"Heterogeneity and evolution rates of delta virus RNA sequences.";
J. Virol. 64:5594-5599(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imazeki F., Omata M., Ohto M.;
"Heterogeneity and evolution rates of delta virus RNA sequences.";
J. Virol. 64:5594-5599(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.0%; Score 39; DB 1; Length 195; 53.8%; Pred. No. 33; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, last sequence update)
01-MAY-1992 (Rel. 22, last annotation update)
Delta antigen.
Pepatitis delta virus (isolate Japanese S-2) (HDV).
Viruses, Daltavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPATITIS DELTA VIRAL INFECTIONS.
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MEDLINE-91012805; Pubmed-2214027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90192; BAA14216.1; -. EMBL; X60193; CAA42749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                         PTM: PHOSPHORYLATED.
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PIR; S18678; S18678.
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CC or send an email to licensediabish.

DR Heris, 1090199; BAR142771; -
DR Heris, 1090296; BAR142771; -
DR Heris, 1090296; BAR142771; -
DR Heris, 1090289; BAR142971; -
DR Heris, 1090289; BAR142971; -
DR PERCORN; BAR14291; HVL-ag; 1.

WA ARLIGAD: NUA-Ag; 1.

SQ SEQUENCE 195 AA: 27912 MA; 27912 MA
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092eag rickettsia
094bt0 arabidopsis
09uet5 homo sapien
09uk1 homo sapien
09uk216 homo sapien
09uk2 homo sapien
09uk2 homo sapien
09uk2 homo sapien
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09uk3 mus musculu
09uk3 mus musculu
09uk3 escherichia
09uk3 escherichia
09uk3 escherichia
09uk4 drosophila
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26.411 Million cell updates/sec
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                                                    August 6, 2002, 17:09:29; Search time 111.35 Seconds
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                                                                                                                                                                           562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                          fotal number of hits satisfying chosen parameters:
                                                                                                                                                        562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
                                   )M protein - protein search, using sw model
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094BT0
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09UNK2
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09D0Y8
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Q9GRG0
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Q9VTN6
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_invertebrate:*
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sp_unclassified:*
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Match Length DB ID
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sp_phage:*
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sp_rodent:*
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092619 homo sapien 0957t2 leishmania 094irl zea mays (m 05526 aquifex aeo 09c031 homo sapien 09h1b homo sapien 09c032 homo sapien 09c032 homo sapien 09c034 homo sapien 09c034 homo sapien 09c034 homo sapien 09c035 homo sapi		0; Gaps 0;	
AA. update) on update) TEIN BSP30)	Hominidae; DDBJ databa B4DB7D CRC6 DB 4; Leng	2e-05; 0;	; 249 AA. ed) sequence update) annotation update)
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50.6 11.49.4 49.7 49.4 49.	Eutheria; Primat ID=9606; FROM N.A. () (JUN-2001) to th 121901; CAC03546.1 249 AA; 27011	al Similarity 10 17; Conservativ SSAWQLAKQKAQEAEKL 	096DR5, 096DR5, 096DR5, 096DR5, 096DR5, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, PAROTID SECHETORY PROTEIN. HOMO Saplens (Human).
177 188 199 199 199 199 199 199 199 199 199	Mammalia N NCB1_Tax N NCB1_Tax N TOB1 PROBLIALE N SUBLIALE N EMBLIALE O SEQUENCE OUETY MALCH	8 5	1D 096DR5; AC 096DR5; DT 01-DEC-20 DT 01-DEC-20 DT 01-DEC-20 DE PAROTIC 20 OS HOMO SAPO

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"A member of the PSP/plunc family of BPI proteins is expressed in the human parotlid gland.";
bunnan parotlid gland.";
EMBL: AF422917; AAL28113.1; -. SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                     0; Gaps
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Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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55.4%; Score 46; DB 16; Length 858;
Best Local Similarity 47.1%; Pred. No. 45;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 83; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaceae;
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SEQUENCE 858 AA; 96290 MW; A18F52B6CD5805AE CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Nature 996:133-140(1998).
Nature 956:133-140(1998).
InterPro: IPR003593; AAA.
InterPro: IPR003593; AAA.subfam.
InterPro: IPR001897; ATP_GTP_A.
InterPro: IPR00187; CLR_AB.
InterPro: IPR001176; CLR_AB.
Pfam: PF00004; AAA: 1.
Pfam: PF00861; ClP_N.
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PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
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                                                                                                                                                                                                                                                                                                                                                           1 SSAWQLAKQKAQEAEKI, 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A.
                                        NCBI_TaxID+9606;
                                                                                                   TISSUE-PAROTID;
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PUTATIVE SUCROSE-PHOSPHATE SYNTHASE.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiphantae; Streptophyta: Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; endicotyledons; core eudicots: Rosidae;

eurosids II; Brassicales; Brassicaeea; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizati Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Sakurai T., Salou M., Seki M., Nayush M., Palm C.J., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Frull Length CDNA of gene F5024_170/AT5920280."; "Frull Length CDNA of gene F5024_170/AT5920280."; "Embl. AXM39911: Aak464015.1; "F227 CENBEL; AXM39911: Aak464015.1; "F227 CENBEL; F227 CENB
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain-specific alternative splicing in a stop codon."; Genomics 53:386-376(1999).
-! SIMILARIPY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
EMBL; AF064243; AAC78610.1; ---
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                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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PRT; 1043 AA
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SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 5.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS50002; SH3; 5.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
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InterPro; IPR002048; EF-hand.
InterPro; IPR00261; EPS15_repeat.
InterPro; IPR001452; SH3.
Pfam; PF00036; efhand; 3.
Pfam; PF00018; SH3; 5.
PRINTS: PR00452; SH3OWAIN.
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PRELIMINARY;
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                                                         094BTO;
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     Q94BT0
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TISSUE-BRAIN;
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                                                                                  0; Gaps
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Aucharcoss C., Fuentes J.J., Casas C., de la Luna S., Alcantara S.,

Arbones M.L., Soriano E., Estivill X., Pritchard M.;

"Alu-splice cloning of human intersectin (ITSN), a putative
multivalent binding protein expressed in proliferating and
differentiating neurons and overexpressed in Down syndrome.";

Eur. J. Hum. Genet. 0:0-0(1999).

Eur. J. Hum. Genet. OrDerre EF-HAND CALCIUM BINDING PROTEINS.

EMBL, AF114488; AAD29953.1;

HSSP; P29355; ISEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    Score 44; DB 4; Length 1220;
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.0%; Score 44; DB 4; Length 1220;
69.2%; Pred. No. 1.4e+02;
tive 2; Mismatches 2; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERSECTIN LONG FORM.
                                                                                                                                                                                                                                                                                                      Q9UNI);
U-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERSECTIN SHORT ISOFORM.
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                                                                                                                                                                                                                                                                               PKT; 1220 AA.
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PROSITE; PS50002; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro: IPR002048; EF-hand.
Interpro: IPR000261; EPS15_repeat.
Interpro: IPR001452; SH3.
                                           53.0%;
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                                  Query Match
Best Local Similarity 69.2%
watches 9; Conservative
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Best Local Similarity 69.2%
Matches 9; Conservative
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                                                                                                                                                                       618 OLOKOKSMEAERL 630
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                                                                                                                              5 QLAKQKAQEAEKL 17
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                 Q9UNK1
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095216
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Gaps
MEDLINE-99017974; PubMed-9799604;

Guipponi M., Scott H.S., Chen H., Schebesta A., Rossier C.,
Antonarakis S.E.;

Antonarakis S.E.;

Two isoforms of a human intersectin (ITSN) protein are produced by brain-specific alternative splicing in a stop codon.";

Genomics S.3.59-376(1998).

-i - SIMILARITY: TO OPHER EF-HAND CALCIUM BINDING PROTEINS.

EMBL: AF064244; AAC78611.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ducharces C., Fuentes J.J., Casas C., de la Luna S., Alcantara S., Arbones M.L., Soriano E., Estivill X., Pritchard M.; Arbones M.L., Soriano E., Estivill X., Pritchard M.; "Alu-splice cloning of human intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome."; EMBL. J. Hum. Genet. 0:0-0:1999).

-: SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. EMBL; AF114487; AAD29952.1;
-: SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. InterPro: IPR000008; C2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1721 AA; 195559 MW; 851A5CFB2BC4EBFC CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM0054; EFD; 2.
SMART; SM00054; EFD; 2.
SMART; SM00023; EFD; 2.
SMART; SM0023; PH: 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00326; SH3; 5.
PROSITE; PSS00014; PLOMAIN, 2; 1.
PROSITE; PSS00013; PH_DOMAIN, 1.
PROSITE; PSS00021; SH3; 5.
                                                                                                                                                                                                                                                                                InterPro: TPR000008; C2.
InterPro: IPR002048; EF-hand.
InterPro: IPR002051; EPS15_repeat.
InterPro: IPR000108; Neu_Cyt_fact_2.
InterPro: IPR001349; PH.
InterPro: IPR001349; RhoGEF.
InterPro: IPR001452; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00018; SH3: 5.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00036; efhand; 3. Pfam; PF00169; PH; 1. Pfam; PF00621; RhoGEF; 1. Pfam; PF00018; SH3; 5.
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Best Local Similarity 69.2°
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 QLAKQKAQEAEKL 17
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                                                                                                                                                                                                                                                            HSSP; P29355; 1SEM.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last segu
01-DEC-2001 (TrEMBLrel. 19, Last anno
                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
EMBL; AK004194; BAB23216.1; -.
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                                                                                                                                                                       1110047B07RIK PROTEIN.
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                                                    Q9D0Y8;
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   09D0Y8
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                                                    MEDLINE-20347328; PubMed-10887074; Walsh P.J., Heltz M.J., Campbell.C.E., Cooper G.J., Medina M., Wang Y.S., Goss G.G., Vincek V., Wood C.M., Smith C.P.; "Molecular characterization of a urea transporter in the gill of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Batrachoididae; Opsanus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 44; DB 4; Length 1721; 69.2%; Pred. No. 2e+02; tive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1721 AA; 195421 MW; FC4DE644D8BEA2BE CRC64;
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EMBL, AF165893; AAD53268.2; ..

Interpro; IPRO0117; Cu-oxidase.

PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.

SEQUENCE 475 AA; 52838 MW; 700E2B180445198C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000261; EPS15_repeat.
InterPro; IPR000108; Neu_cyt_fact_2.
                                           InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001452; SH3.
PFam; PF00168; C2: 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00169; PH: 1.
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Matches 9; Conservative
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-GILL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=95145;
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SEQUENCE

ααααααααααααααααααααααα

Query Match

09PUQ5; Q9PUQ5

OUFFFERSOUSZKOXKEFFKKO

ESULT 10

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-C578L/6J; TISSUE-EMBRYO;

Kawai J., Shihadawa A., Shibada K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fokuda S.,

Alaxawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fokuda S.,

Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alazawa T., Saito T., Saito T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Banalov S., Casavant T.,

Kadota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Webtiguez I., Sakamoto N.,

A Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J., Achtumn M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moules S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup A).
Bacteria; Proceobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13658 MW; C024F28F8A5B016A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10).
METG OR NMA0275.
17, Last sequence update)
19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 5K PA GENE ENCODING PENICILLIN ACYLASE, SEGMENT 1 PRECURSOR
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                NCBI_TaxID-562;
                                                                                                                                      Escherichia.
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                                                          (FRAGMENT)
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SEQUENCE
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Q9GRG0
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023362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96020635; PubMed-8577256;
Loessner M.J., Wendlinger G., Scherer S.;
"Heterogeneous endolysins in Listeria monocytogenes bacteriophages: a new class of enzymes and evidence for conserved holin genes within the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                          HISSP, POUVS9; HURA.

INTERPRO; PRO01142; LRNA-Synt_I.

INTERPRO; IPRO02304; LKNA-Synt_met.

INTERPRO; IPRO02347; LKNA-bind.

Pfam; PF01588; LKNA, bind; L.)

PRINTS; PR01041; TRNASYNTHMET.

PR057TE; PS00178; AA TRNA_LIGASE_I; 1.

PR057TE; PS00178; AA TRNA_LIGASE_I; 1.

SEQUENCE (885 AA; 76984 MW; 07F045915ED3BEF3 CRC64;
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EMBL; AJ242593; CAB53816.1; -.
SEQUENCE 125 AA; 14707 MW; AF95EFFAE323ADF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Mol. Microbiol. 16:1231-1241(1995).
meningitidis Z2491.";
Nature 404:500-506(2000).
EMBL: ALI62752; CAB83583.1; -.
HSSP; P00959; IMEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 WELAKOEGODA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 WQLAKQKAQEA 14
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Eukaryota: Alveolata: Ciliophora: Oligohymenophorea: Hymenostomatida:
Tetrahymenina: Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The CDNA sequences of three tetrins, the structural proteins of the Tetrahymena oral filaments, show that they are novel cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                  MEDLINE-85236066; PuhMed-2989404;
Bruns W., Hoppe J., Tsai H., Bruening H.J., Maywald F., Collins J.,
Escherichia coli.
Bacteria; Proteobacteria: gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                        27 >227 POTENTIAL.
27 >235 POTENTIAL.
290 >350 POTENTIAL.
350 As; 38903 MW; 1D97970699A751DC CRC64;
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Profist 151:171-180(2000).
EMBL, A276471; CACO7819-1; -.
SEQUENCE 731 AA; 87196 MW; A2FC64972BF06BE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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Brimmer A., Weber K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
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736 AA

PRT;

PRELIMINARY;

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Or 0.3336;
TO 0.3347.998 (TrEMBLEE). 05, Created)
TO 0.3347.998 (TrEMBLEE). 05, Last sequence update)
TO 0.3M1.9998 (TrEMBLEE). 17, Last amotation update)
ENTRY 0.1998 (TrEMBLEE). 17, Last amotation update)
TO 0.1M1.2001 (TrEMBLEE). 17, Last amotation update)
NATGIOSON.
NATGIOSON.
ATANGIOSON.
AND IN BRANCETTI.
BENTE.
AND LINE-98121113; PubMed-9461215;
AND LINE-8812113; PubMed-94812113;
AND LINE-8812113; PubMed-94812113;
AND LINE-8812113; PubMed-9481213;
AND LINE-8812113; PubMed-94812113;
AND LINE-8812113; PubMed-9481213;
AND LINE-881213; AND LINE-881213;
AND LINE-881213; AND LINE-881213;
AND LINE-881213; AND LINE-881213;
AND LINE-881213; AND LINE-8
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0; Gaps

50.6%; Score 42; DB 10; Length 736; Illarity 53.3%; Pred. No. 1.7e+02; Conservative 3; Mismatches 4; Indels

Query Match Best Local Similarity Matches 8; Conserva Search completed: August 6, 2002, 17:09:30 Tob time: 932 sec

2 SAWQLAKQKAQEAEK 16 |||:|||:|||: 422 SAWKLAKLNSNEATR 436

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Location/Qualifiers
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AAG54
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2. SIDSI/gegdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
4. SIDSI/gegdata/hold-geneseqy-geneseqp-embl/AA1982.DAT:*
5. SIDSI/gegdata/hold-geneseqy-geneseqp-embl/AA1984.DAT:*
6. SIDSI/gegdata/hold-geneseqy-geneseqp-embl/AA1984.DAT:*
7. SIDSI/gegdata/hold-geneseqy-embl/AA1986.DAT:*
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Human gene 5 encod
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SH3D1A prote
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13.629 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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                                                                                           August 6, 2002, 16:52:52; Search time 138.55 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             747574 segs, 111073796 residues
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                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                US-10-020-139-2_COPY_68_84
83
                                                           OM protein - protein search, using sw model
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AAB24069
AAB25765
AAB75351
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AAB94691
AAY32158
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AAE04203
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Maximum DB seq length: 2000000000
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Match Length DB
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8833
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846
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Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Drosophila melanog
S. pneumoniae prot
Drosophila melanog
Neisseria gonorrhe
Trypanosoma cruzi
                                  Streptococcus pyog
Wild type penicill
V567 mutant penicil
F248 mutant penici
F24V mutant penici
F24L mutant penici
Sequence encoded b
A. faecalis.E. col
Drosophila melanog
                                                                                    Polypeptide sequen
Enterococcus faeca
Pseudomonas aerugi
Arabidopsis thalia
          human diagno
     prote
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                                                                                                                                                                    Trpanosoma cruzi a
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polypeptide,
SH3D1A prote
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                                       AAW57840
AAW57843
AAW57844
                                                                                   AAU07884
AAU35024
AAU36302
                                                                                                                 AAG54285
ABB58344
ABB58317
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ABB70070
                                                                                                                                           AAY74342
AAW19086
                             AAY32155
AAY50199
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1204
4286
                                                      AAW57845
                         AAY32156
                                                                     AAB37817
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                                                                AAP61009
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Searched:

Run on:

Database

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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                               /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                               "mature hPSP"
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Result Š.

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18-SEP-1998
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Sednence
                                                                                                                                                                              AAW60682;
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NW60682
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Claim 1; Fig 1A-C; 65pp; English.
      gastrointestinal tissues
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          δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretory tissue; gastrointestinal tissue; HPSP, Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancrealitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or
                                                            New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parotid secretory protein; human; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 83; DB 19; Length 249; 100.0%; Pred. No. 5.9e-05; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parotid secretory protein (HPSP).
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                                                                                                                                          Claim 16; Fig 1; 94pp; English
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Best Local Similarity 100.
Matches 17; Conservative
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WPI; 1998-377651/32.
N-PSDB; AAV44759.
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N-PSDB; AAV37699.
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This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, of salivary gland, thyroid, castrointestinal tract or pancreas. Slorger's syndrome, of saves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, orbn's disease and atrophic gastriits. Host cells to roduce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP mad for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect these ending sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ,
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100.0%; Pred. No. 5.9e-05;
tive 0; Mismatches 0;
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99US-0141037.
99US-0143048.
99WO-US28313.
99WO-US30911.
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25-JUN-1999;
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                                                                                                                                                                                                                                           one of the human PRO proteins designated PRO212, PRO290, PRO314, PRO515, PRO619, PRO6117, PRO619, PRO6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skelteral muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Altheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Caps
                                                                                                               Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer \cdot
                                                                                                                                                                                                                            that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 21; Length 249; 100.0%; Pred. No. 5.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                                                                                              The present invention describes an isolated antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SEQ ID #77.
                                                                                                                                                                                   Claim 61; Fig 26; 286pp; English.
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Best Local Similarity 100.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      septic shock; impotence.
    Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                WPI; 2000-572270/53.
                                                                        N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200037491-A2.
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This sequence represents a human secreted protein amino acid sequence.
The invention relates to sequences AAAB7725-88774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides.

Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for claim from the sequence of the cDNAs sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The CDNAs may also be useful in diagnostic, forensic, gene proteins. The CDNAs may also be useful in diagnostic, forensic, gene cherapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention are discasted to treat discases including canner, autoimmune diseases, cardiovascular disorders, cystic fibrosis, bypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, alherosclerosis, neurodegenerative disorders, garf rejection, Alzheimer's disease, consultative disorders, garf rejection, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                   Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                               Bougueleret L, Dumas J, Duclert A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Figure 10; 306pp; English.
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99US-0141032
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                               mapping procedures -
                                                                                                                                                                                                                       WPI: 2000-442637/38.
                                                                                                                                                                                                                                                               N-PSDB; AAA87727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                      49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples - \,
                                                                                                                                                                The present invention relates to 49 Secreted proteins and the CDNAS encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                   100.0%; Score 83; DB 22; Length 249; 100.0%; Pred, No. 5.9e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          Indels
  Jobert S;
Dumas Milne Edwards J, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ JD NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25745 standard; Protein; 260 AA.
                                                                                                                                Claim 10; Page 281; 307pp; English
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological disorder.
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                                      WPI; 2001-071487/08
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                                                                                                                                                                                                                                                                     Sednence
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                                                                                                                                                                                                                                                                                                                   Query Match
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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antinfbummatic; cells they are expressed in, such as: antinflammatory; antipheumatic; cells they are expressive; antibacterial; endocrine; cardiant; central mervous system; virucide; antianglede; antimutagen; cardiants; cardianes; dermatological; antialergic; antiastummatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; rytostatic; neuroprotective; antidepressant; nootropic; cardiant been can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, panceatiis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoiett disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, asthma, diabetes, cancer, multiple sclerosis, depression, and allored and allored cardiactions and allor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Gaps
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Claim 20; Page 260; 1217pp; English.
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2000US-0180628.
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2000US-0216880.
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2000US-0209467
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Best Local Similarity 100.
Matches 17; Conservative
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2000US - 02182 2000US - 02209 2000US - 02245 2000US - 02245 2000US - 02252 2000US - 02252	2000US-0226819. 2000US-0226881. 2000US-0226881. 2000US-0229824. 2000US-0229344. 2000US-0229344. 2000US-0229344. 2000US-0229345. 2000US-0229345. 2000US-0229345. 2000US-0229345. 2000US-0229345. 2000US-0239346. 2000US-0239381. 2000US-0231249. 2000US-0231249. 2000US-023399. 2000US-0239937. 2000US-0239937. 2000US-0239937. 2000US-0239937. 2000US-0239937.	2000US-024180 2000US-024180 2000US-024182 2000US-024461
	12 - AUG - 2000 22 - AUG - 2000 23 - AUG - 2000 01 - SEP - 2000 01 - SEP - 2000 01 - SEP - 2000 01 - SEP - 2000 05 - SEP - 2000 06 - SEP - 2000 08 - SEP - 2000 08 - SEP - 2000 09 - SEP - 2000 14 - SEP - 2000 15 - SEP - 2000 16 - SEP - 2000 17 - SEP - 2000 18 - SEP - 2000 19 - SEP - 2000 10 - SEP - 2000 27 - SEP - 2000 28 - SEP - 2000 29 - SEP - 2000 20 - CCT - 2000	-OCT-200 -OCT-200 -OCT-200
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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2000US-0246475
2000US-02464775
2000US-0246477
2000US-0246477
2000US-0246478
2000US-0246523
2000US-0246525
2000US-0246526
2000US-0246526
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2000US-0246619
2000US-0246619
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2000US - 024 9207
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2000US - 024 9210
2000US - 024 9211
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2000US-0256719.
2000US-0251479.
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2000US-0251990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11-DEC-2000; 2000US-0254097
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N-PSDB; AAK63229.
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06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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17-NOV-2000;
17-NOV-2000;
                                             08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17 - NOV - 2000;
17 - NOV - 2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
                                                                                                     08-NOV-2000;
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Claim 11; SEQ ID NO 18041; 3071pp + Sequence Listing; English.

AAX54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the

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protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheunatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; asisease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psordasis; sepeis; diaberes; etherosclerosis; cardiovasqular disorder; applogenic disorder; kidney disorder; endorder; pregnancy-related disorder; gene therapy; cell culture; chemoraxis; food additive; binding partner identification.
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; proliferative disorder; cancer; tumour;
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                                                                                                                                                                        Score 46; DB 22; Length 85; Pred. No. 8.1;
                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Komatsoulis GA, Baker KP, Young PE;
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 436-437; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AAE04203 standard; Protein; 123 AA.
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                                                                                                                                                                          55.4%;
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                                                                                                                                                                                                              Conservative
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es 8; Conserva
                                                                                                                        85 AA;
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                                                                                                                          Seguence
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                                                                                                                                                                            Query Match
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The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, heamatopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, diabetes, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to subure of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in the disorders mantioned above, and the disorders mantioned above, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foctal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy, neurological disorder; Alzheimmer's disease; Parkinson's disease; cognitive disorder; schizophrenia; astima; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; proliferative disorder; cancer; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||| :|| || ::
90 awqlrqqklqeeqr 103
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Homo sapiens.

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AAD08488-AAD08529 represent CDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE0429 represent human secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. CC treating or ameliorating medical conditions can be diagnosed by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of abnormalities, haematopoietic disorders, disease of the immune system, and include developing products for the diagnosis or treatment of print of alsorders, disease, control mutation, alsorders, endicates, and information, sepsis, diabetes, atherosclerosis, string and estimated disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound the disorders specific for a protein of the invention can be used in also as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunososays e.g., radioimmunossay or enzyme linked immunosasay e.g., radioimmunossay or enzyme linked immunosasay e.g., radioimmunosasay or enzyme in human axx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition \cdot
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                                                                                                                                                                                                                             Ruben SM, Komatsoulis GA, Baker KP, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 453; 509pp; English.
                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                              19-NOV-1999; 99US-0166415.
30-JUN-2000; 2000US-0215136.
                                                               15-NOV-2000; 2000WO-US31162.
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Best Local Similarity 5/...
From Similarity 5/...
From Similarity 5/...
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                                                                                                                                                                                                                                                                       WPI; 2001-343793/36.
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    25-MAY-2001.
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 1'-end sequence of the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH1842 represent human cDNA sequences; AAB92446 to AAH3639 represent human amino acid sequences; and AAH33629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         Otsuki T;
                                                                                                                                                                                                                                                                                                                                          Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 15659; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                      sogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32158 standard; Protein; 641 AA.
                                                                                                                                                                                             27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                                                                                                            99.JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.28;
                                                                                                                                                                                                                                                         09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present invention.
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                                                                                                                                                                                                                                                                                                  (HELLI-) HELLIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581 qlqkqksmeaerl 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SH3D1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 595 AA;
                                                                                                                                                                                                                                                                                                                                        Isogai T,
                                                       EP1074617-A2.
                                                                                                                                                                            29-JUL-1999;
                                                                                               07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                           Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32158;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy.

Human protein sequence SEQ ID NO:15659.

26-JUN-2001 (first entry)

AAB94691;

AAB94691 standard; Protein; 595 AA,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the protein encoded by the human SH3DIA CDNA clone 9 (see AAZ4574). SH3DIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The cromosome 21. The protein includes SH3 domains and EH domains, chromosome 21. The protein includes SH3 domains and the latter chromosome 21. The protein includes SH3 domains and the latter with maintenance of the cytoskeleton. At least 3 isoforms of SH3DIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, che diagnosis and treatment of megakaryocytic abnormality. The invention providers in chromosome 21, low platelets in deletion for 21, association of chromosome 21, low platelets in deletion for 21, association of chromosome 21, low platelets in deletion for 21, association of chromosome 21, with leukaemias, neural abnormalities, dysfunctions and disorders in louding brain malformations and consistive dysfunctions, microcephaly, ilssencephaly, and colpocephaly Methods are also provided: for suppressing challs the provints of the provints of the corresponding cognitive dysfunctions are severally expressing challs the provints of the corresponding reasons are also provided: for suppressing challs the provints of the corresponding cognitive dysfunctions corresponding reasons and also provided: for suppressing challs are also provided: for suppressing challs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and
                  SH3D1A; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; patalete disorder; neural disorder; thrombocytopenia; haematopoletic disorder; cognitive dystinction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells unable to regulate themselves; screening for a somatical teration in the SH301A gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyjc abuormality, myeloproliferative disorder, haematopoletic disorder, platelet disorder; or leukaemia; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.0%; Score 44; DB 20; Length 641; Best Local Similarity 69.2%; Pred. No. 1.3e+02; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening of drugs for cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       (CEDA-) CEDARS SINAI HEALTH SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANM93229 standard; Protein; 642 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 15; 99pp; English.
                                                                                                                                                                                                                                                                                                                   99WO-US08371.
                                                                                                                                                                                                                                                                                                                                                                        98US-0082007
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|| 115 qlqkqksmeaer| 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korenberg JR, Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-633829/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ34574
                                                                                                                                                                                                                      W09953062-A2.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                   16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                        16-APR-1998;
                                                                                                                                                                                                                                                                        21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia
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<u>></u>:
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been should and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA asily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3D1A; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                       Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 2647; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.0%; Score 44; DB 22; Length 642; 69.2%; Pred. No. 1.3e+02; tive 2; Mismatches 2; Indels
                                                 Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32157 standard; Protein; 648 AA.
           Human polypeptide, SEQ ID NO: 2647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use in genetic manipulation -
                                                                                                                                                                                                                                               2000JP-0118774.
                                                                                                                                                                                           07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                  02-MAY-2000; 2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAK94139
                                                                                                                                                                                                                              08-JUL-1999;
                                                                                      Homo sapiens.
                                                                                                                      EP1130094-A2
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                                                                                                                                                                                                                                                 11-JAN-2000;
                                                                                                                                                           05-SEP-2001
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30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167

11-OCT-2001

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Nucleic acid from the human SH3D1A gene and its products, useful for
the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Dis sequence represents the protein encoded by the numan shalled of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on chromosome 21. The protein includes SH3 domains and EH domains, both associated with protein includes SH3 domains and the latter with maintenance of the cytoskeleton. At least 3 isoforms of SH3DA exist (see AAY32154-58). The invention provides methods for myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder acute leukaemia, chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcophaly, lissencephaly, methods are also provided: for suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tunner risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoletic disorder, platelet disorder or leukaemia; and
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the protein encoded by the human SH3DlA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening of drugs for cancer therapy.
                                                                                                                                                             (CEDA-) CEDARS SINAI HEALTH SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Fig 13; 99pp; English.
                                                                                                                        98US-0082007.
                                                                                99WO-US08371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 glgkgksmeaerl 630
                                                                                                                                                                                                      Korenberg JR, Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                              WP1; 1999-633829/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AA234573.
W)9953062-A2.
                                                                              16-APR-1999;
                                                                                                                        16-APR-1998;
                                       21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The useful for chromosome polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reacting disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and portant contains and polynucleotide sequences have applications in the polynomial partners or other traits to assess biodiversity and processing of the contains and polynucleotide sequences have applications in the polynomial partners or other traits to assess biodiversity and processing of the contains and polynucleotide expensions or other traits to assess biodiversity and processing contains and polynucleotide activity.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

WPI; 2001-639362/73. Drmanac RT, Liu C,

N-PSDB; AAS84762

(HYSE-) HYSEQ INC.

The invention relates to isolated polynucleotide (I) and

Claim 20; SEQ 1D No 50934; 103pp; English.

biodiversity

and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published\_pct\_sequences.

932 AA:

Sequence

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Gaps
                                         ..
53.0%; Score 44; DB 22; Length 932; 69.2%; Pred. No. 1.9e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                             AAM43519 standard; Protein; 1035 AA.
                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 197.
                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
                  Local Similarity 69.2 les 9; Conservative
                                                                                                            158 glgkgksmeaerl 170
                                                                         5 QLAKQKAQFAEKL 17
                                                                                                                                                                                                                                                    AAM43519;
                      Best Loca
Matches
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Query Match
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cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiallergic; hepatotropic; antidiabetic; antibacterial; antinflammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human
Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
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Human; chromosome mapping; gene apping; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

WO200175067-A2. Homo sapiens.

Novel human diagnostic protein #20566.

13-FEB-2002 (first entry)

ABG20575;

ABG20575 standard; Protein; 932 AA.

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24-FEB-2000; 2000US-018662B.
26-AMAR-2000; 2000US-018662B.
16-AMAR-2000; 2000US-0186874.
17-MAR-2000; 2000US-0189123.
19-AMAY-2000; 2000US-0198123.
19-AMAY-2000; 2000US-0198123.
19-AMAY-2000; 2000US-0198123.
11-JUL-2000; 2000US-0216135.
11-JUL-2000; 2000US-0216137.
11-JUL-2000; 2000US-0216127.
11-JUL-2000
                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01309
                                                                                WO200155308-A2.
                             Homo sapiens.
                                                                                                                                           02-AUG-2001.
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26 - SEP - 200 27 - SEP - 200 27 - SEP - 200 29 - SEP - 200 29 - SEP - 200 29 - SEP - 200 29 - SEP - 200 02 - OCT - 200 02 - OCT - 200 02 - OCT - 200 02 - OCT - 200 03 - OCT - 200 03 - OCT - 200 04 - 200 05 - OCT - 200 06 - OCT - 200 07 - OCT - 200 07 - OCT - 200 07 - OCT - 200 08 - OCT - 200 08 - OCT - 200 09 - OCT - 200 09 - OCT - 200 01 - OCT - 200 01 - OCT - 200 02 - OCT - 200 03 - OCT - 200 04 - OCT - 200 05 - OCT - 200 06 - OCT - 200 07 - 2	10.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 20.0077-2000 08.NOV-2000	08 - NOV - 200 17 - NOV - 200	01-DEC-2000 05-DEC-2000 05-DEC-2000 05-DEC-2000 06-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000
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(AUMA-) HUMAN GENOME SCI INC.
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488781/53.

N-PSDB; AAI63825

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders  $^{\circ}$ 

Claim 11; SEQ ID NO 197; 664pp + Sequence Listing; English.

The invention relates to human polynucleotides (AA163803-AA164012) and the invention relates to human polynucleotides (AA163803-AA164012) and the encoded proteins (AAM34497-AAM3660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists or are useful in the diagnosis, treatment and prevention of: (a) cancer, c.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uroganital; (b) immune discretes e.g. Addison's disabetes mellitus, c.c. conditis, (c) cardiovascular disorders such as myccardial ischaemias; c.c. collis, (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Con the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.Wipo.int/Pub/published\_pct\_sequences.

Sequence 1035 AA;

0; Gaps 53.0%; Score 44; DB 22; Length 1035; 69.2%; Pred. No. 2.2e+02; tive 2; Mismatches 2; Indels ( Ouery Match 53.0 Best Local Similarity 69.2 Matches 9; Conservative

5 QLAKQKAQEAEKL 17  $\stackrel{\sim}{\sim}$  629 giqkqksmeaerl 641

Search completed: August 6, 2002, 16:52:53 Job time: 335 sec

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12, Appl
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13, Appl
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Sequence 143, App
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8.107 Million cell updates/sec
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Sequence 35, A
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Sequence 43,
Sequence 13,
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                                                                            August 6, 2002, 16:53:54; Search time 51.22 Seconds
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/cgn2_6/ptodata/2/laa/AA_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-285-957-33
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US-08-541-780-6
US-08-541-780-6
US-08-557-3098-27
US-08-894-780-27
US-08-993-674A-27
US-08-993-674A-27
US-08-993-674A-27
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US-08-857-3098-43
US-08-857-3098-43
US-08-857-3098-12
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US-08-820-980-12
US-08-820-980-12
US-08-820-980-12
US-08-820-980-12
US-08-820-980-12
US-08-820-980-13
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                                                                                                                                                                                                                          231628 seqs, 24425594 residues
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                                                   OM protein - protein search, using sw model
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83
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: McDonnell Boehnen Hulbert & Berghoff: 300 South Wacker Drive Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                      US-09-355-166-9
US-08-553-436A-6
US-09-336-447A-76
                                                                                                          US-08-272-255-7
PCT-US95-08565-7
US-08-356-354-6
US-08-356-354-4
US-08-778-656-6
US-08-778-656-4
                                    US-08-961-083-102
US-09-095-855-196
US-08-408-095-21
                                                                                                                                                                                    US-08-905-223-395
US-09-042-428-2
US-08-964-127-4
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41.2%; Pred. No. 64;
tive 5; Mismatches
                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03249
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/793,229
FILING DATE: 23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              : Sequence 34, Application US/08793229
; Patent No. 5891703
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 41.2 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSAWQLAKQKAQEAEKL 17
/ MOLECULE TYPE: protein US-08-793-229-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U:
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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1 SNMWVIGKNKAQDAKAI 17

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50.6%; Score 42; DB 3; Length 555; 41.2%; Pred. No. 64; tive 5; Mismatches 5; indels
                                                                                                      APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: OUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/285,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DALL:
ATTORNEY/AGENT INFORMATION:
                                      Sequence 34, Application US/09285957
Patent No. 6033823
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/793,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/08793229 Patent No. 5891703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 970
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: protein
5-09-285-957-34
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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ESULT 2
S-09-285-957-34
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5-08-793-229-33
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Gaps
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41.2%; Pred. No. 64;
Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SQUUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                          SOFTWARE: Patentin redease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,229 FILING DATE: 23-APR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,957
                                                                                                                                              FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03249
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          97075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09285957
Patent No. 6033823
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/793,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 9707
TELECOMMUNICATION INFORMATION:
TELEFANE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 41.2%;
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-793-229-33
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-285-957-33
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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290 SNMWVIGKNKAQDAKAI 306

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Query Match 557; Guery Match 557; Best Local Similarity 41.2%; Pred. No. 64; Matches 7; Conservative 5; Mismatches 5; Indels
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41.2%; Pred. No. 98;
Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) COMENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Misset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
:: FIVE PALO ALTO SQUARE, 4TH FLOOR
PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLAUSING DATE: 13710307
CLAUSING DATE: 13710307
PRIOR APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/00US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/07731157A; Patent No. 5457032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: ATCC 21285
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 844 amino acids
                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 41.2#
Matches 7; Conservative
                                                                                                                                                                                                                        1 SSAWQLAKQKAQEAEKI, 17
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-957-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          US-07-731-157A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Gaps
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Pred. No. 98;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25 (EPO)
                                                                                APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Wan der Laan, Jan M.
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                              ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GENO-027/00US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
FILING DATE:
APPLICATION NUMBER: EP 90200962
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Sequence 5, Application US/07731157A ; Patent No. 5457032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Kluyvera citrophila
(S-08-541-780-6
                    . Sequence 6, Application US/08541780
; Patent No. 5935831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Van der Laan, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: '6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 415-494-7622
415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                         94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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US-08-541-780-6
                                                                                                                                                                                                                                                                                                                     COUNTRY:
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1 SSAWOLAKOKAQEAEKL 17

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                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/731,157A
FILING DATE: 19910509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Mono
APPLICANT: Wan der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
ITILE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                             CORRESPONDENCE ADURESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE, 4TH FLOCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Haug, H
AUTHORS: Buckel, P
AUTHORS: Bock, A
TITLE: Penicillin acylase from E.coli: unique
TITLE: gene-protein realion.
JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/COCKET NUMBER: GRO-027/00US
TELECOMMUNICATION INFORMATION:
TELECAM: 415-494-7622
TELETAX: 380916 COOLEY PA
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
FILLIG DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 846 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schumacher, G
Sizmann, D
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Best Local Similarity 41.2.
Best Local 7; Conservative
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                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                              CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 5713-5727
DATE: 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                              94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-07-731-157A-5
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 8
S-08-541-780-5
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION ON NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·,
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                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
               ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Bock, A
TITLE: Penicillin acylase from E.coli: unique
JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: RAE-VENTER PH.D. BARBARA
REGISFRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GRKO-027/00US
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PAPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
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; Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 846 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: | : | || |: | 290 SNMWVIGKSKAQDAKAI 306
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Sizmann, D
                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 41.2
7; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
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                                                     PALO ALTO
CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protoRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 5713-5727
DATE: 1986
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                                                                                                                  94306
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US-08-557-309B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
AUTHORS:
                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
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                                                                           STATE:
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PREVENTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Mchaell, Patricia D.
ATILE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                          ::
                                                                                                                                                                                                                47.6%; Score 39.5; DB 3; Length 40; 60.0%; Pred. No. 10; tive 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210121.42202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-DEC-1997
CLASSFFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 27, Application US/08993674A ; Patent No. 6228372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ 1D NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
                                                                    40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        Conservative
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APPLICATION NUMBER: US
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                  3 AWQLAKOKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                         111 1:::11 111:
22 AWQEAEERAQREAEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AWQLAKQKAQ-EAEK 16
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22 AWQEAEERAQREAEE 36
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Washington
                                                                                                                                                                                            Query Match
Best Local Similarity
9, Conserve
                                                                                      amino acid
                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-993-674A-27
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                                                                                                        STRANDEDNESS:
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US-08-993-674A-27
                                                                                                                                TOPOLOGY:
                                                                                                                                                  US-08-834-306-27
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                                                                    LENGIH:
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                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.6%; Score 39.5; DB 2; Length 40; 60.0%; Pred. No. 10; tive 4; Mismatches 1; Indels
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY IJ.P
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY FACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           CLASSIPLATION DATE: US/08/557,309B FILING DATE: 14-NOV-1995 CLASSIPLATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MAKI, IDAVID J. REGERATOROMBRER: 31,392 REFERENCE/DOCKET NUMBER: 210121.422 TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104-7092
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08834306
Patent No. 6054135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 40 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AWQLAKOKAQ-EAEK 16
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                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-557-3098-27
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Matches 9; Conserv
                                                                                                      98104-7092
               STREET: bove contraction seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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US-08-834-306-27
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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PREVENTION OF
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Patent No. 6228372

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mouthon, Raymond L.
APPLICANT: Mouthon, Raymond L.
APPLICANT: Mouthon M.
APPLICANT: Mouthon M.
APPLICANT: Mouthon W.
APPLICANT: Mouthon W.
APPLICANT: Mouthon W.
APPLICANT: MONEIL!
APPLICA
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                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 50; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.6%; Score 39.5; 1
60.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFACE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 186 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 186 amino acids TYPE: amino acid
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||| AWQEAEERAQREAEE 125
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Best Local Similarity
5, Conserva
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Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                          FILING DATE: 15
CLASSIFICATION:
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TOPOLOGY: 11
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US-08-993-674A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TILE, OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 186;
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 39.5; [60.0%; Pred. No. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210121.422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
                                                      Sequence 43, Application US/08557309B Patent No. 5916572
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/08834305 Patent No. 6054135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 amino acids
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||11 AWQEAEERAQREAEE 125
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                 STREET: bocc
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98104-7092
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(ESULT 12)
1S-08-557-309B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
S-08-557-309B-43
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-08-834-306-43
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US-08-993-674A-43

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1; Gaps
                      47.6%; Score 39.5; DB 4; Length 186; 60.0%; Pred. No. 50; Live 4; Mismatches 1; Indels 1
                                                                                                                                                                                                                                              Sequence 13, Application US/09185160
Patent No. 652137
GNERAL INFORMATION:
APPLICANT: ODELL, JOAN T.
APPLICANT: HARDER, PATRICIA A.
TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR FROM PHASEOLUS
TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR FROM PHASEOLUS
UNMERS PONDENCES: 14
CORRESPONDENCE S: 14
CORRESPONDENCE ADDRESS:
                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: FRH PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,459
FILING DATE: NOVEMBER 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REPRENCE/DOCKET NUMBER: BB-1096
TELEPHONE: 302-992-4926
INFORMATION FOR SEQ. 1D NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/185,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 734 amino acids
TYPE: amino acid
STRANDEDNESS:
Ouery Match
Best Local Similarity 60.00
Best Local 9; Conservative
                                                                                                                                 ||| ||:::|| |||:
||| AWQEAEERAQREAEE || 15
                                                                                                    3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : TOPOLOGY: linear
: MOLECULE TYPE: peptide
JS-09-185-160-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19898
                                                                                                                                                                                                          RESULT 15
US-09-185-160-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                            QQ
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Commence of Proper Processing Service

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Ouery Match
Best Local Similarity 52.9%; Pred. No. 2.98+02;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

1 SSAWQLAKQKAQE-AEK 16
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iearch completed: August 6, 2002, 16:53:55
 ob time: 287 sec

<sup>||:| :| |:| |||</sup> 76 SSSWAWLKSDAEEDAEK 92

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

dun on:

August 6, 2002, 17:05:15 ; Search time 66.51 Seconds (Without alignments) 13:003 Million cell updates/sec

US-10-020-139-2\_COPY\_115\_123 Perfect score: litle:

1 EPIDDGKGL 9 scoring table:

283138 segs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 searched:

'otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 2000000000

Ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	cripti	fatty acid/phospho	بو		E	NADP-dependent mal	Conserved hypothet	H+-transporting AT	probable ABC trans	0 (0)		. –	3 1	N-isopropylammelia	hypothetical prote	topolsomerase IV	, a	? ?	2 2	7300	topolsomeras	topoisomeras		2			•	GDD dissociation i		บร
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	Score	44	40	38	37	37	36	36	36	36	35	32	35	35	35	35	35	35	35	32	32	35	35	32	35	34	34	34	34	34
esu]t	NO.	1	7	m	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ογ qq hypothetical protein F32B6.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Toot-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C;Accession: T21644
R;Basham, V.
R;Basha

A;Map position: 4 A;Introns: 22/2; 61/1; 141/2; 176/3; 200/3; 290/3; 332/1

A; Gene: CESP: F32B6.9

C; Genetics

32
33 34 69.4 447 2 A54091  34 34 69.4 448 2 S36746  35 34 69.4 468 2 G86453  36 34 69.4 656 2 T08293  37 34 69.4 656 2 T08293  38 34 69.4 656 2 T08293  39 34 69.4 656 2 T08293  40 34 69.4 721 2 A56352  40 34 69.4 721 2 A56352  41 34 69.4 721 2 A56352  42 34 69.4 721 2 A56352  44 5 34 69.4 721 2 A56352  45 69.4 723 2 AD0203  46 69.4 1061 2 T13107  47 34 69.4 1061 2 T13107  48 69.4 1061 2 T13107  48 69.4 1139 2 B70954  49 4 34 69.4 1139 2 B70954  40 4 34 69.4 1139 2 B70954  41 34 69.4 1139 2 B70954  42 34 69.4 1139 2 B70954  44 33 67.3 134 2 D97401  ALIGNMENTS  ALIGNM
34
35 34 69.4 464 2 G86453 YUP 36 34 69.4 665 2 T01673 37 34 69.4 665 2 T01673 38 34 69.4 665 2 T01673 39 34 69.4 765 2 T01673 39 34 69.4 723 2 AD0203 40 34 69.4 723 2 AD0203 41 34 69.4 723 2 AD0203 42 69.4 723 2 AD0203 43 4 69.4 723 2 AD0203 44 34 69.4 1061 2 B81447 44 34 69.4 1061 2 B70954 44 34 69.4 1139 2 B70954 44 34 69.4 1139 2 B70954 44 34 69.4 1139 2 B70954 45 33 67.3 134 2 D97401  ALIGNMENTS  RESULT ALIGNAE SPECIES AS AS AS DECENDED FOR TYPHI ANGRET HAND SPECIES AS AS AS DECENDED CALLED SECONAR TYPHI ANGRET HAND SPECIES AS AS AS DECENDED CALLED SECONAR TYPHI C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang C.Accession: A10641 C.Accession: A10641 C.Accession: A10641 C.Accession: A10641 C.Accession: A10641 A.Authors: Parry, G.; James, K.D.; Thomson, N.R.; Pickarth, T.; Connerton A. Mall B. S.; O'Gaoza, P.; Conin, A.; Davies, P.; Davies, R.M.; Don, A.; Title: Complete genome sequence of a multiple drug resistant A.; Accession: A10641 A.;
### 1979   1979
38 34 69.4 662 2 G88451  39 34 69.4 721 2 A56352  40 34 69.4 721 2 A56352  41 34 69.4 721 2 A56352  42 34 69.4 769 2 B81447  43 34 69.4 1061 2 T13107  44 34 69.4 1061 2 T13107  44 34 69.4 1062 2 T13107  44 34 69.4 3263 2 E82410  ALIGNMENTS  RESULT  AIGNACHIA  ALIGNMENTS  RESULT  AIGNACHIA  ALIGNMENTS  RESULT  AIGNACHIA  ALIGNMENTS  ALIGNMENTS  RESULT  AIGNACHIA  ALIGNMENTS  ALIGNACHIA  ALIGNMENTS  ALIGNACHIA  A
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41 34 69.4 769 2 BB1447 che 42 34 69.4 1061 2 T13107 tai 43 34 69.4 1061 2 E870954 44 34 69.4 1061 2 E870954 44 34 69.4 1061 2 E870954 44 34 69.4 1061 2 E82410 hypp 45 33 67.3 134 2 D97401  ALIGNMENTS  RESULT ALGORIT ALGORIT GLETY acid/phospholipid synthesis protein Plsx [imported] - Sa C; Species: Salmonella enterica subsp. enterica serovar Typhil C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang C; Accession Alofal C; Date: 09-Nov-2001 #text_chang C; Accession Alofal A; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickar, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M; Don Nature 413, 848-882, 2001 A; Authors: Parry, C; Quail, M; Rutherford, K.; Simmonds, M; A; Accession: Alofal A; Status: preliminary A; Accession: Alofal A; Residues: 1-359 - RAR A; Residues: 1-359 - RAR A; Gene: STY1231 A; Gene: STY1231
42 34 69.4 1061 2 T13107 tai 43 34 69.4 11310 2 E870954 44 34 69.4 11319 2 E870954 44 34 69.4 11319 2 E870954 44 34 69.4 11319 2 E870954 44 35 67.3 134 2 D97401  ALIGNMENTS  RESULT fatty acid/phospholipid synthesis protein Plsx [imported] - Sa C:Species: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Accession: Al0641 R:Parkhill, J.: Dougan, G.: James, K.D.: Thomson, N.R.: Plockarth, T.: Connerton, P.: Cronin, A.: Davis, P.: Davies, R.M.: Dougan, G.: James, K.D.: Thomson, N.R.: Plockarth, T.: Connerton, P.: Cronin, A.: Davis, P.: Davies, R.M.: Dougan, G.: Atthors: Parkhors: Parry, C.: Quail, M.: Rutherford, K.; Simmonds, M.: A:Authors: Preliminary A:Accession: Al0641 A:Accession: Al0641 A:Accession: Al0641 A:Accession: Al0641 A:Accession: Al0641 A:Accession: Al0642 A:Accession: Al0641 A:Acce
A139 2 B70954 hyp 43 34 69.4 1139 2 B70954 hyp 44 34 34 69.4 129 2 B97401 hyp 45 33 67.3 134 2 D97401 hyp ALIGNMENTS  RESULT A1064 bloospholipid synthesis protein PlsX [imported] - Sa C:Species: Salmonella enterica subsp. enterica serovar Typhi A:NOCE: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang-C:Accession: A10641
RESULT 1 ALIGNMENTS  RESULT 1 ALIGNMENTS  RESULT 1 ALIGNMENTS  RIC: Species: Salmouella enterica subsp. enterica serovar Typhi A: Worke: this species has also been called Salmonella typhi C: Species: Salmouella enterica subsp. enterica serovar Typhi A: Worke: this species has also been called Salmonella typhi C: Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_changre; Accession: Aloula, J: Dougan, G: James, K.D.; Thomson, N.R.; Pickarth, T.; Connerton P: Cronin, A.; Davis, P:; Davies, R.M.; Dov, S.; Moule, S: O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov, S.; Moule, S: O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davies, P.; Davies, M.; A.; Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; A.; Accession: Alosoule rype: DNA A; Residues: 1-359 - FARA A; Residues: 1-359 - FARA A; Residues: 1-359 - FARA A; Cross-references: GB: AL513382; PIDN: CADO8316.1; PID: g1650236; C: Genetics: Tayl231
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RESULT 1 Alighments ALIGNMENTS ALGALY acid/phospholipid synthesis protein Plsx [imported] - Sa C: Species: Salmonella enterica subsp. enterica serovar Typni A: Note: this species has also been called Salmonella typhi C: Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_chang C: Accession - AloGal
RESULT 1 A10641 A10641 A10641 A10641 A10641 Fatty acid/phospholipid synthesis protein Plsx [imported] - Sa C; Species: Salmonella enterica subby enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_changy C; Accession: A10641 R; Parkhill, J: Dougan, G: James, K.D.; Thomson, N.R.; Pickar, th, T: Connerton, P: Cronin, A: Davis, P.; Davies, R.M.; Dougan, E.; Moule, S.; O'Gaora, P. A; Muthors: Parry, C: Quail, M.; Rutherford, K.; Simmonds, M.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Accession: A10641 A; Accession: A10641 A; Setzence number: A80502; PMID:11677608 A; Molecule type: DNA A; Residues: 1-359 - APAR> A; Cross-references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236; C; Genetics: A; Gene: STY1231
A10641 fatty acid/phospholipid synthesis protein Plsx [imported] - Sa Cisty acid/phospholipid synthesis protein Plsx [imported] - Sa Cisty acid/phospholipid enterics subsp. enterica serowar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang. C;Accession: A10641 R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickar, Lh, T; Connerton, P; Cronin, A; Davis, P.; Davies, R.W; Pickar, S; O'Gaora, P. A; Moule, S; O'Gaora, P. A;Authors: Parry, C; Quail, M; Rutherford, K; Simmonds, M; Aritle: Complete genome sequence of a multiple drug resistant A;Accession: A10641 A;Accession: A10641 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-359 - APAR> A;Cross-references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236;C;Genetics:
fatty acid/phospholipid synthesis protein Plsx [imported] - Sa Cispecies: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang C:Accession A10641 R:Parkhill, J:Dougan G.; James, K.D.; Thomson, N.R.; Pickarth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dougan G.; Accession, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dickarth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dougan G.; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A. Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A. Accession. A10641 A. Stetus: preliminary A. Molecule type: DNA A. Residues: 1-359 - PARR> A. McCross-references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236; C:Genetics:
C:Species: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang C:Accession: A10641 R:Parkhilli, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickart th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Don Nature 413, 848-852, 2001 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A:Title: Complete genome sequence of a multiple drug resistant A:Accession: A10641 A:Accession: A10641 A:Accession: A10641 A:Accession: A10641 A:Accession: A10641 A:Accession: A10641 A:Residues: 1-359 A-PAR> A:Residues: 1-359 A-PAR> A:Cross-references: GB:AL513382; PIDN:CAD08316.1; PID:g16502365 C:Genetics:
Cloate: 09-vo-2001 #sequence_revision 09-Nov-2001 #text_chang-cloate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang-Cloate: 09-Nov-2001 #text_chang-Cloate: 09-Nov-2001 #text_chang-cloatesion: Alougan, G.; James, K.D.; Thomson, N.R.; Pickarth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Don, S.; Moule, S.; O'Gaora, P.; Croin, A.; Davis, P.; Davies, R.M.; Don, A. Huthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A. Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A. Accession: AloGal, Alogal, A. Accession: Alogal, Alogal, Alogal, Alogal, Alogal,
C. Accession: A106H R.Parkhill, J. Dougan, G.; James, K.D.; Thomson, N.R.; Pickart, T.; Connerton P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov, Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Accession: A1062, PM1D:11677608 A; Accession: A10641 A; Status: Preliminary A; Molecule Pype: DNA A; Residues: 1-359 < PAR> A; Cross-references: GB: AL513382; PIDN: CAD08316.1; PID: g1650236; G: Genetics: A; Gene: STY1231
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickar, th, T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Do, S.; Moule, S; O'Gaora, P. Nature 413, 848-852, 2001 A; Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: A80502; PMID:11677608 A; Reference number: A80502; PMID:11677608 A; Recession: A10641 A; Setus: preliminary A; Molecule type: DNA A; Residues: 1-359 - APAR> A; Gross references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236; A; Gene: STY1231
Ln, 'I. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dov. S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A/Title: Complete genome sequence of a multiple drug resistant. A.Reference number: AB0502; PMID:11677608 A.Accession: A10641 A.Status: prediminary A.Molecule type: DNA A.Residues: 1-359 - APAR> A.Gross references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236: C.Genetics: A.Gene: STY1231
Nature 413, 448-852, 2001 A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A.Itle: Complete genome sequence of a multiple drug resistant A.Reference number: AB0502; PMID:11677608 A.Accession: A10641 A.Actaus: preliminary A.Molecule type: DNA A.Residues: 1-359 ACAR> A.Gross-references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236; C.Genetics: A.Gene: STY1231
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: A80502; PMID:11677608 A; Accession: A10641 A; Setaus: preliminary A; Molecule type: DNA A; Residues: 1-359 < APAR> A; Cross references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236: C:Genetics: A; Gene: STY1231
A.Title: Complete genome sequence of a multiple drug resistant. A.Reference number: AB0502; PMID:11677608 A.Accession: A10641 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-359 <
A.Accession: A10641 A.Status: preliminary A.Molecule Vype: DNA A.Residues: 1-359 < PAR> A.Cross-references: GB:AL513382; PIDN:CAD08316.1; PID:g1650236; A.Gene: STY1231
PIDN:CAD08316.1;
PIDN:CAD08316.1;
PIDN:CAD08316.1;
PIDN:CAD08316.1;
A GENE STATE
C;Superfamily: phospholipid synthesis protein
Ouery Match 89.8%: Score 44: DB 2: Tenath 350.
Similarity 77.8%; Pred. No. 0.99;
vative 2; Mismatc

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R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heldelberg, B.; Laub, M.T.; DeBsoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4166-4141, 2001
A.;Tille: Complete Genome Sequence of Caulobacter crescentus.
A.;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein PA3421 [imported] - Pseudomonas aeruginosa (strain PAG C; Species: Pseudomonas aeruginosa (strain PAG C; Species: Pseudomonas aeruginosa (strain 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: A83218 R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adman, S.; Yaun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; H. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c; Species: Lactobacilius case;
C; Date: 22 Nov-1993 #sequence_revision 03-Aug-1995 #text_change 19-Jan-2001
C; Accession: S309: W.; Baeuerlein, E.; Schleifer, K.H.
R; Klugbauer, N.; Ludwig, W.; Baeuerlein, E.; Schleifer, K.H.
Syst. Appl. Microbiol. 15, 323-330, 1992
A; Title: Subunit beta of adenosine triphosphate synthase of Pectinatus frisingensis a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004763; GB:AE004091; NID:g9949556; PIDN:AAG06809.1; GSPDB:GN
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A:Residues: 1-470 <KLU>
A:Coss-references: EMBL:X64542; NID:943971; PIDN:CAA45840.1; PID:943972
C:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase
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C;Genetics:
C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C.Accession: C87689
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2; Mismatches
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                     preliminary
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Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis Reference number: 217011; MUID:97271300
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Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
Reference number: AB1807; MUID:21595285; PMID:11759840
Accession: AE2118
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akazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A Res. 8, 205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                                /pothetical protein 21 - Orgyia pseudotsugata nuclear polyhedrosis virus
Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
:Accession: T10290
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                                                  Score 40; DB 2; Length 413;
Pred. No. 6.9;
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7689
2P-dependent malic enzyme [imported] - Caulobacter crescentus Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.6%; Score 38; DB 2; Length 627;
87.5%; Pred. No. 26;
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                                                                                                       0; Indels
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                                                                  100.0%; Pred. No. v.,
rive 0; Mismatches
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                                                  81.6%;
                                                                           Local Similarity 100.0
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Matches 7; Conservative
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Best Local Similarity
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Residues: 1-428 <KUR>
                                                                                                                                                                                                                      384 PIDDGKG 390
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                                               Query Match
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Dysobletical protein ytcG - Bacillus subtilis
Nylothetical protein ytcG - Bacillus subtilis
C.Species: Bacillus subtilis
C.Accession: Dosgog, AZG580
C.Accession: Dosgog, AZG580
C.Accession: Bacillus S.Berullus, C.V.; Edylania, K.M.; Alloni, G.; Azevedo, V.; Be
C.Species: Bacillus S.Berullus, C.V.; Caldwell, B.; Capunno, V.; Carter, N.M.;
A.Bern, S., Broullett, S., Bruillat, K.D.; Erington, J.; Fabret, C.; Ferrari,
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galett, J.; Handod, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Houlo,
Noceter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Luu, H.; Masuda, S.; May
Y.; Mantors: Lauber, J.; Lazarevic, V.; Ex, Sence, B.; Seklageri, J.; Satowaka, A.; Sakouchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Seklagchi, J.; Sakowaka, A.; Sakouchi, M.; Tanakoshi, A.; Tanaka, H.; Terpstra, P.; Tognoni, A.; Tosaro, V.; Uchiy
T.; Minters, P.; Wilpett, A.; Yanamoto, H.; Yasumoto, K.; Yasumoto, K.; Yasumoto, M.; Yata, K.; Yosumoto, M.; 
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C:Species: Bacillus
C
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Pred. No. 23;
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C;Superfamily: conserved hypothetical protein HI0943
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Local Similarity 62.5%;
nes 5; Conservative
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'Date: 15.5ep-2000 #sequence_revision 15.5ep-2000 #text_change 31-Dec-2000

'Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoquchi, S.D.; Warrener, P.; Hickey, M.J.; Br

dman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

ature 406, 959-964, 2000
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:Reference number: A82950; MUID:20437337
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;Residues: 1-5627 <STO>
;Cross-references: GB:AR004673; GB:AE004091; NID:99948501; PIDN:AAG05850.1; GSPDB:GN001
;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :Species: Streptomyces coelicolor
;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
;Keywords: ATP biosynthesis; hydrolase; nucleotide binding; P-loop
;155-162/Region: nucleotide-binding motif A (P-loop)
;181-350/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; bubatted to the EMBL Data Library, April 1998; Reference number: 221571
;Reference number: 221571
;Accession: T35192
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                                                                                                                                                                                                         73.5%; Score 36; DB 2; Length 470; 66.7%; Pred. No. 48; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%; Score 36; DB 2; Length 744; 62.5%; Pred. No. 78; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
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87.5%;
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Best Local Similarity 87.5%
                                                                                                                                                                                                                                            Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity
''ns 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 DPIDDGEAL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: SCOEDB:SC5B8.08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
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                                                                                                                                                                                                                  Query Match
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71.4%; Score 35; DB 71.4%; Pred. No. 63;
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Best Local Similarity 7/...
The conservative
                                        Ouery Match
Best Local Similarity 71.4%
Matches 5, Conservative
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Best Local Similarity
6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           579 EPINDGKFL 587
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66 EVIDDGRGM 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: F35D11.2
                                                                                                                                                                                                                 42 PVEDGKG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                             2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: G82078
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Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum Reference number: A97359; PMID:11743194
                                                                       Residues: 1-387 KKUN>
Cross-references: GB:299124; GB:AL009126; NID:y2636442; PIDN:CAB16064.1; PID:g2636574
Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I age, G.; Glillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Tence 294, 2317-23<u>2</u>3; 2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Reference number: Ab2577; PMID:11743193
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                            Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Agrobacterium tumefaciens
Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drolase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                     Ouery Match
71.4%; Score 35; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.4%; Score 35; DB 2; Length 397; 71.4%; Pred. No. 63; 0; Indels ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                 Gene: yycP
Superfamily: Bacillus subtilis hypothetical protein yycP
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Map position: linear chromosome
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Map position: linear chromosome
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Best Local Similarity
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Residues: 1-397 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 PTDDGKG 191
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                                                      Molecule type: DNA
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Accession: D70090
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A; Molecule type: DNA
A; Residues: 1-614 <FUL>
A; Cross-references: EMBL:U29381; NID:9868214; PID:9868216; PIDN:AAA68749.1; CESP:F35D
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MuID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    topoisomerase IV, chain B VC2431 [imported] - Vibrio cholerae (strain N16961 serogrou
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0
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C;Date: 20-Sep-1999 *Sequence_revision 20-Sep-1999 *text_change 20-Sep-1999
C;Accession: T16268
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82078
                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 2; Length 614; 77.8%; Pred. No. 99;
DB 2; Length 400;
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                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F35Dll.
A;Reference number: 218487
A;Accession: T16568
                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F35D11.2 - Caenorhabditis elegans
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                                                                  2; Mismatches
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search completed: August 6, 2002, 17:05:16
Tob time: 918 sec

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(without alignments)
10.598 Million cell updates/sec
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P43242 oryctolagus
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045435 caenorhabdi
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                                                             August 6, 2002, 17:07:35; Search time 32.88 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50396
P24322
P24322
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P27176
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P17133
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P05879
Q92072
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                      otal number of hits satisfying chosen parameters:
                                                                                                                                                                                105224 seqs, 38719550 residues
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GD1A_MOUSE
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RRPL_PUUMH
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	ALIGNMENTS			
P15885 ruminococcu	BGLS_RUMAL	947 1	65.3	45 32
Q09263 caenorhabdi	YOD3_CAEEL	359 1	65.3	44 32
O88398 mus musculu	ADVL_MOUSE	319 1	65.3	43 32
P47161 saccharomyc	YJ96_YEAST	311 1	65.3	42 32
Q9ulw8 homo sapien	PDI3_HUMAN	564 1	65.3	41 32
043058 schizosacch	SEP1_SCHPO	563 1	65.3	40 32
	KPK1_PHAVU	509 1	65.3	39 35
P46367 saccharomyc	DHA4_YEAST	519 1	65.3	38 32
P09431 rhodobacter	NTRB_RHOCA	356 1	65.3	37 32
_	HO2_HUMAN	316 1	65.3	36 35
P23711 rattus norv	HO2_RAT	315 1	65.3	35 32
O70252 mus musculu	HO2_MOUSE	315 1	65.3	34 32

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihla M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Daviss R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609; MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhimurium; STRAIN-LT2; MEDLINE-89137265; PubMed-9642179; Zhang Y., Cronan J.E. Jr., Zhang Y., Cronan J.E. Jr., Transcriptional analysis of essential genes of the Escherichia coli fatty acid biosynthesis gene cluster by functional replacement with the analogous Salmonella typhimurium gene cluster."; J. Bacteriol. 100:3295-3303(1998).
                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fatty acid/phospholipid synthesis protein plsx. PLSX OR STW1192 OR STY1231.
                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; Pubmed-11677608;
                                                                                                                                                                                 Salmonella typhimurium, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
                                          STANDARD;
                                                                                                                                                                                                                                                             NCBI_TaxID-602, 601;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                    Salmonella typhi.
                                          PLSX_SALTY
                                                                                                                                                                                                                                             Salmonella.
PLSX_SALTY
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STANDARD;
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les 7; Conserv
                                                                                                                                                                                        NCBI_TaxID=164623;
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                   Y023_NPVOP
010282;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
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Fatty acid biosynthesis: Phospholipid biosynthesis; Complete proteome.
SEQUENCE 359 AA; 38716 MW; ADD01BA971D5ECD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                             89.8%; Score 44; DB 1; Length 359; 77.8%; Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
Hypothetical 49.0 kDa protein F32B6.9 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 413 AA; 48965 MW; A66E69A83C78790B CRC64;
                                                                                                                                                                                                                                                                                                                             Pred. No. 0.31;
2; Mismatches
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100.0%; Pred. No. 2...
                                                                                                                     EMBL; AF044668; AAC38647.1; ALT_INIT.
EMBL; AE008751; AAL20121.1; -.
EMBL, AL627269; CAD08316.1; -.
StyGene; SG110682; PISX.
InterPro; IPR003664; FA_synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR000615; Worm_fam_8 Pfam; PF01062; Worm_family_8; I. Probom; PD002802; Worm_fam_8; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z81074; CAB03043.1; -.
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.69
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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345 EPLDDGKGV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                               Query Match
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40\_CAEEL

SULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                 "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klugbauer N., Ludwig W., Bauerlein E., Schleifer K.H.; "Subunit beta of adenosine triphosphate synthase of Pectinatus frisingenesis and Lactobacillus casei."; Syst. Appl. Microbiol, 15:323-330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                             Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL 73.1 KDA PROTEIN.; 3B81055F4C27F8E4 CRC64;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-297271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.6%; Score 38; DB 1; Length 657;
87.5%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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                                            01.NOV-1997 (Rel. 35, Created)
16.cCT-2001 (Rel. 40, Last sequence update)
16.cCT-2001 (Rel. 40, Last sennotation update)
Hypothetical 73.1 kDa protein precursor (ORF21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATPB_LACUA STANDARD; PRT; 470 AA. 003234; 01-007-1993 (Rel. 27, Created) 01-00T-1993 (Rel. 27, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
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PRT;
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SEQUENCE 657 AA; 73128 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U75930; AAC59020.2; -
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                                                                                                                                                                                               Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus casei.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Brotherton P.M., Barth P.T.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94043292; PubMed=8227000;
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                                                             EMBL; AF008220; AAC00357.1; -.
                                                                               299118; CAB14860.1; -. M15183; AAA22403.1; -.
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62...
Best Local Similarity 62...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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STRAIN~K12 / MC1655;
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                                                                                                                                                                                                                                                                                                                                 2 PIDDGKGL 9
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-far European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBDANTS: ALPHA(3), BETA(3), GAMAMA(1), DELTA(1), EPSILON(1), CF(0) HAS THREE MAIN SUBDINTS: A, B AND C.
-i - SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoshino T., McKenzie T., Schmidt S., Tanaka T., Sueoka N.; "Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for DNA replication initiation and membrane attachment."; Proc. Natl. Acad. Sci. U.S.A. 84:653-657(1987).
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470 AA; 51457 MW; 2258AF44C6DE13FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; ATP synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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HSSP: P07677; 1SKY.

Interpro; IPR004100; ATP-synt_ab_N.

Interpro; IPR000793; ATPase_AB_C.

Interpro: IPR000194; ATPase_alpha_beta.
                                                                                                                                                                                                                                                                                                                                                           pfam; prococos; ATP-synt_ab; 1. Pram; prococos; ATP-synt_ab; 1. Pfam; prococos; ATP-synt_ab; 1. Prococos; 3. Prococos; ATP-synt_ab; 1. PROSITE; PSO0152; ATPASE_ALPHA_BETA; 1.
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MEDLINE=87118226; PubMed=3027697;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrogen ion transport. NP_BIND 155 162
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98 DPIDDGEAL 106
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Kato J.-I., Nishimura Y., Imamura R., Niki H., Hiraga S., Suzuki H.;
"New topoisomerase essential for chromosome segregation in E. coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Escherichia coli topoisomerase IV. Purification, characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                        71.4%; Score 35; DB 1; Length 152; 62.5%; Pred. No. 7.4;
1.ve 2; Mismatches 1; Indels
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                                                  EMBL; miller, BG1383; ytcg.
Subtilist; BG1383; ytcg.
Interpo; IPR003796; bUr193.
Pfam; PF02644; bUF193; 1.
Hypothetical protein; Complete protecome.
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                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PARE OR NFXD OR B3030.
                                                                                                                                                                                                                                                                                                                                                            630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Springer A.L., Schmid M.B.;
Nucleic Acids Res. 21:1805-1809(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit structure, and subunit intera
J. Biol. Chem. 268:24481-24481(1993).
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MEDLINE=91261812; PubMed-8388096;
Springer A.L., Schmid M.B.;
"Molecular characterization of the Salmonella typhimurium parE gene.";
Nucleic Acids Res. 21:1805-1809(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                     PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> H (IN QUINOLONE-RESISTANT STRAIN
allele of the parE gene encoding a subunit of topoisomerase IV.", Antimicrob. Agents Chemocher. 41.175-179 (1997).
-!- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
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Isomerase; Topoisomerase; ATP-binding; Antibiotic resistance;
                                                                                     OF A CIRCULAR DNA MOLECULE.
SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE.
SIMILARITY: BELONGS TO THE TYPE II POPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%; Score 35; DB 1; Length 630; 66.7%; Pred. No. 33; 1; Indels ative 2; Mismatches 1; Indels
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01-MAR-2002 (Rel. 41, Last annotation update)
Topoisomerase IV subunit B (EC 5.99.1.-).
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InterPro; IPR00228B, DNA_topoisoII.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR001394; HATPase_C.
Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 1.
Pfam; PF002518; HATPase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0418; TPI2FAMILY.
ProDom; PD000616; DNA_topoisoII; 1.
ProDom; PD149633; DNA_gyraseB_C; 1.
                                                                                                                                                                                                                                                                                             EMBL; MS8409; AAA24298.1; ALT_SEQ.
EMBL; U28377; AAA69198.1; -.
EMBL; AE000385; AAC76066.1; -.
BMEL; L22026; AAC36841.1; -.
PIR; B36075; B36075.
HSSP; P06982; 1AJ6.
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01-MAR-2002 (Rel. 41, Last sequ
01-MAR-2002 (Rel. 41, Last anno
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SMART; SM00433; TOP2c; 1.
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Best Local Similarity 66.7%
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MEDLINE-1554947; PubMed-11677608;
MEDLINE-1554947; PubMed-11677608;
MEDLINE-1554947; PubMed-11677608;
MEDLINE-1554947; PubMed-11677608;
MEDLINE-1554947; PubMed-11677608;
MEDLINE-155497; PubMed-11677608;
MINGHER C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Cronin A., Davis P., Davis P., Chillingworth T., Connerton P., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
W
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-> S (IN TS MUTANT PARE377).
-> P (IN TS MUTANT PARE493).
                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Couttney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                 Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
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PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
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-!- SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE.
-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                          SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
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-> P (IN REF. 1).
-> R (IN REF. 1).
7F2FCC25EBB30019 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD000616; DNA_copoisoll; 1.
Prodom; PD149633; DNA_copraseB_C; 1.
SMART; SM00387; HATPASe_C; 1.
SMART; SM00433; HOP2C; 1.
PROSITE; PS00177; TOPOISOMERASE_II: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L05544; AAA27182.1; -
EMBL; AE607846; AAL22055.1; -
EMBL, A662727; CA003013.1; -
PTR; S33711; S33711.
HSSP; P06982; 1AJ6.
StyGene; SG10277; pare.
Interpro; IPR00228; DNA_topoisol1.
Interpro; IPR001241; DNA_topoisol1.
Interpro; IPR001354; HATPASSE_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00986; DNA_gyraseB_C; 1.
Pfam: PF00204; DNA_LOPDISO11; 1.
Pfam: PF02518; HATPASE_C. 1.
PKINTS; PR00418; TP12FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 AA;
SEQUENCE FROM N.A.
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1 EPIDDGKG 8
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P21856;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (GGPPSASE)
(Geranylgeranyl diphosphate synthase) [Includes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBSEQUENT BINDING OF GTP TO THEM.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                          01-0c7-1996 (Rel. 34, Created)
1-0c7-1996 (Rel. 34, Last Sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Score 34; DB 1; Length 323; 100.0%; Pred, No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Skeletal muscle;
STRAIN-BALB/C; TISSUE-Skeletal muscle;
MEDLING-941,17740; PubMed-7513052;
Shishava A., Suedhof T.C., Czech M.P.;
"Cloning, characterization, and expression of a novel GDP dissociation inhibitor isoform from skeletal muscle.";
Mol. Cell. Bolo. 14:3459-3468(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                               323 AA.
                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD, MGI:99846; Gdil.
InterPro; IPR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; 1
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                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPase activation.
                                            66 EVIDDGRGM 74
                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10090;
            1 EPIDDGKGL 9
                                                                                                                                                                                                                                                OR RABGDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 EPIDDG 269
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                                                                                                                             GDIA_MOUSE
P50396;
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P2432:
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                                                                                             ESULT 8
DIA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1) (SMG P25A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10); Farnesyltranstransferase (EC 2.5.1.29)].
AL-3 OR ALBINO-3.
                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                          Carattoli A., Romano N., Ballario P., Morelli G., Macino G.;
"The Neurospora crassa carotenoid biosynthetic gene (albino 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00348; polyprenyl_synt; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
PROSITE; PS00723; POLYPRENYL_SYNTHET_1: 1.
Carotenoid biosynthesis; Isoprene biosynthesis; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -: SUBCELLULAR LOCATION: Cytoplasmic.
-: INDUCTION: BY BLUE LIGHT.
-: SIMILARITY: BELONGS TO THE FPP/GGPP SYNTHETASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels
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7989DEEABD8E360F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                  STRAIN=74-OR23-1A;
MEDLINE=91170267; Pubmed=1826006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 AA; 47887 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                          Neurospora crassa.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 EDIDDGRG 400
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                                                                                           "Molecular cloning and characterization of a novel type of regulatory protein (GDI) for smg p25A, a ras p21-like GTP-binding protein."; Mol. Cell. Biol. 10:4116-4122(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROFIENS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM.
SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99019719; Pubmed=9802909;
Chen W., Feng Y., Chen D., Wandinger-Ness A.;
"Rebl1 is required for trans-golgi network-to-plasma membrane
transport and a preferential target for GDP dissociation inhibitor.";
Mol. Biol. Cell 9:3241-3257(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
MEDLINE-90318376; PubMed-2115118;
Matsui Y., Kikuchi A., Araki S., Hata Y., Kondo J., Teranishi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96196507; PubMed=8609986; Schalk I., Zeng K., Wu S.-K., Stura E.A., Matteson J., Huang M., Tandon A., Wilson I.A., Balch W.E.; "Structure and mutational analysis of Rab GDP-dissociation inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 1; Length 447; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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SEQUENCE 447 AA; 50565 MW; 69C68B03BDC1BA3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA.
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                                                                                                                                                                                                                                                                                                                                                                                            [3]
X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS).
                                                                                                                                                                                                                          SIMILARITY TO CHOROIDERAEMIA PROTEIN.
                                                                                                                                                                                                                                                          MEDLINE=91270365; PubMed=1904992; Fodor E., Lee R.T., O'Donnell J.J.; "Analysis of choroideraemia gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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100.08; Pre
0; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90103; BAA14134.1; -.
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PRINTS; PR00891; RABGDIREP.
                                                                                                                                                                                                                                                                                                                                                                Nature 351:614-614(1991).
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SEQUENCE FROM N.A.
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097555;
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IA_CANFA
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-:- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM.
-:- SUBCELLULAR LOCATION: CYLOPISSMIC (By similarity).
-:- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sedlacek Z., Konecki D.S., Korn B., Klauck S.M., Poustka A.;
"Evolutionary conservation and genomic organization of XAP-4, an Xq28
located gene coding for a human rab GDP-dissociation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RABA GDP dissociation inhibitor alpha (RAB GDP dissociation inhibitor alpha (RAB GDP).
GDII OR RABGDIA OR XAP4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96311563; PubMed=8733135;
Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,
Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
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[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF027360; AAD04246.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00891; RABGDIREP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                      INHIBITOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98282090; PubMed-9620768; D'Adamo P., Menegon A., Lo Nigro C., Grasso M., Gulisano M., Tandon A., Tandon A., Tandon A., Yaltorta F., Blenvenu T., Gedeon A.K., Oostra B., Wu S.-K., Tandon A., Valtorta F., Balch W.E., Chelly J., Toniolo D.; "Mutations in GDI1 are responsible for X-linked non-specific mental retardation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98334551; PubMed=9668174; Blenvenu T., Des Porties V., Salit Martin A., McDonell N., Billuart P., Carrie A., Vinet M.-C., Couvert P., Toniolo D., Ropers H.-H., Moraine C., van Bokhoven H., Fryns J.-P., Kahn A., Beldjord C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93359978; PubMed=7543319; Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A., "Expression patterns of two human genes coding for different rab GDP-dissociation inhibitors (GDIs), extremely conserved proteins involved in cellular transport.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Non-specific X-linked semidominant mental retardation by mutations
                                                                                                                                                                                                                                                                                                                               Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.; Wandekerckhove J., "Microsequences of 145 proteins recorded in the two-dimensional gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DISEASE: DEFECTS IN GDI1 ARE THE CAUSE OF X-LINKED NON-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MENTAL RETARDATION (XLMR). SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a Rab GDP-dissociation inhibitor.";
Hum. Mol. Genet. 7:1311-1315(1998).
-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBSEQUENT BINDING OF GTP TO THEM.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: BRAIN; PREDOMINANT IN NEURAL AND SENSORY
                                                                                                                                                                                                                                                                                                                                                                                         protein database of normal human epidermal keratinocytes."
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                             Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in cellular transport.";
Hum. Mol. Genet. 4:701-708(1995).
                                                                                                                                                                                                                                                                                           TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed~1286667;
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EMBL, X79355, CAA55909.1; JOINED.
EMBL, X79356, CAA55909.1; JOINED.
EMBL, X79357, CAA55909.1; JOINED.
EMBL, X79358, CAA55909.1; JOINED.
EMBL, X79359, CAA55909.1; JOINED.
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                                                                                                    SEQUENCE OF 143-181 FROM N.A.
                                                                                                                                                                                     SEQUENCE OF 328-436 FROM N.A.
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SEQUENCE FROM N.A.
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                                          Strausberg R.;
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                    FISSUE-Lung
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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/FILd=VAR.008130.
R -> P (IN XLMR).
/FILd=VAR_008131.
D -> G (IN REF. 2).
N -> K (IN REF. 2).
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Shisheva A., Suedhof T.C., Czech M.P.;
"Cloning, characterization, and expression of a novel GDP
dissociation inhibitor isoform from skeletal muscle.";
Mol. Cell. Biol. 14:3459-3468(1994).
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G -> V (IN REF. 5).

H -> Q (IN REF. 5).

D -> G (IN REF. 5).

F -> S (IN REF. 2).

F -> S (IN REF. 2).
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPase activation, Disease mutation.
VARIANT 92 92 L -> P
X79360; CAA55909.1; JOINED.
X79364; CAA55909.1; JOINED.
X79361; CAA55909.1; JOINED.
X79362; CAA55909.1; JOINED.
X79363; CAA55909.1; JOINED.
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Pfam; PF00996; GD1; 1.
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36 N
151 NF
347 G
409 H
442 D
442 D
50582 MW;
                                                                                                                                                                                    X79353; CAA55908.1; -.
L44140; AAA92648.1; -.
BC000317; AAH00317.1; -.
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                                                                                                                                                                                                                                                                                              U14623; AAA21558.1; -. D45021; BAA08078.1; -. L05086; AAC15851.1; -.
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416
442
447 AA;
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Matches 6; Conserv
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388 EPIDDG 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 300104; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 309541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase 6 (EC 2.7.1.-) (Extracellular signal-regulated kinase 3) (ERK-3) (MAP kinase isoform p97) (p97-MAPK).
                                                                                                                                   -i - FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Fetal skeletal muscle;
MEDIINE=595059049; Pubmed=7969157;
Shu A.x., Zhao Y., Mollar D.E., Filer J.S.;
"Cloning and characterization of p97MAPK, a novel human homolog of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                 TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                         Caillol N., Pasqualini E., Lloubes R., Lombardo D.;
"Impairment to file salt-dependent lipase secretion in human
panoreatic tumoral SOJ-6 cells.";
J. Cell. Biochem. 79:628-647(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 34; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D -> Y (IN REF. 1).
G -> S (IN REF. 2).
S -> P (IN REF. 2).
; 58384671991DF793 CRC64;
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                                                                                                                                                                             SUBSEQUENT BINDING OF CTP TO THEM.
                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 14:8202-8211(1994)
                                      MEDLINE=20453283; PubMed=10996854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002005; Rab_GDI_REP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Smooth muscle;
MEDLINE=97030046; PubMed=8875998;
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EMBL; AF130987; AAD25536.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 AA; 50536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X74402; CAA52413.1; -.
SEQUENCE OF 81-439 FROM N.A.
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nes 6; Conserv
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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Cloning, sequencing and expression of the L5, L21, L27a, L28, S5,
S9, S10 and S29 human ribosomal protein mRNAs.":
Biochim. Biophys. Acta 1262:64-68(1995).
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             *Primary structure, expression and chromosomal locus of a human homolog of rat brk3."

Oncogene 13:1575-1579(199)

I FUNCTION: PHOSPHORYLATES MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2).

MAY PROMOTE BUTRY IN THE CELL CYCLE (BY SINILARITY).

TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE SKELETAL MUSCLE. FOLLOWED BY THE BRAIN: ALSO FOUND IN HEART, PLACENTA, LUNG, LIVER, PRACREAS, KIDNEY, AND SKIN FIBROBLASTS.

PANCREAS, KIDNEY, AND SKIN FIBROBLASTS.

**SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

MAP KINASE SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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DAA3AAA9B98BB31F CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Last annotaation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Meloche S., Beatty B.G., Pellerin J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95290496; PubMed=7772601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82680 MW;
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SMART; SM00220: S TKc;
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Matches 5; Conserv
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P46779;
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SEQUENCE
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0; 0; Gaps Query Match 67.3%; Score 33; DB 1; Length 136; Best Local Similarity 66.7%; Pred. No. 16; Matches 6; Conservative 1; Mismatches 2; Indels 2; Indels

1 EPIDDGKGL 9 > 0

earch completed: August 6, 2002, 17:07:36 ob time: 878 sec

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Q926d3 rhizobium m
Q9hyi4 pseudomonas
O69995 streptomyce
Q9fzu3 neisseria m
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09v3z6 drosophila
09sfe7 arabidopsis
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O38236 human immun
O38238 human immun
                                                       August. 6, 2002, 17:09:30 ; Search time 111.35 Seconds (without alignments) 13:983 Million cell updates/sec
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Q93cc8 staphylococ
Q9niu2 drosophila
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q98H58 P88400 Q20040 Q20040 Q9KPD9 Q9KPD9 Q9KPD9 Q9KPD9 Q9KPD9 Q9KPD9 Q9KPD9 Q9KPD9 Q9B231 Q9B231 Q9B231 Q3	99ADQ4 0940940 094D94 99VE7 99CS5 99CX5 091Y71 24349 99VHJ8	PRT; Created) Last seq Last ann SALIVAR; Crania: Calarri EMBL/GenE	NG TANK	
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Staphylococcus aureus.
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Q9W5R8;
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"Mutation of an alternative sigma factor in the cyanobacterium nostoc punctiforme results in increased infection of its symbiotic plant partner, anthoceros punctatus.";
J. Bacteriol. 180:4938-4941(1998).

MEROPS; 541.002;
InterPro: IPR001478 PDZ.
InterPro: IPR001478 PDZ.
InterPro: IPR001581: TSPc.
SMART: SM00228: PDZ: 1.
PROSTIE: PS50106; PDZ: 1.
                                                                                                                                                                                                Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OCT-2001).
EMBL, AF432917: AAL28113.1:
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0\$; Score 49; DB 4; Length 249; Best Local Similarity 100.0\$; Pred. No. 0.28; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Cyanobacteria: Nostocales: Nostocaceae: Nostoc.
NCBL_TaxID=63737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CARBOXYL TERMINAL PROTEASE.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYPOTHETICAL 18.1 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC29133;
MEDLINE=98406048; Pubmed=9733698;
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                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-PAROTID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nostoc punctiforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 EPLDDGSGL 352
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Y1P6 OR CG17489.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                            Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V., Schlievert P.M.;
Schlievert P.M.;
Staphylococcus aureus pathogenicity island 3 (SaP13).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Bybothetical protein.
Hypothetical protein.
SEQUENCE 152 AA, 18082 MW; 17A63018DE9B9AB3 CRC64;
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77.6%; Score 38; DB 2; Length 152;
Best Local Similarity 87.5%; pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roxstrom-Lindquist K., Faye 1.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195190; AAF27819.;
FlyBase; FB91004061; yip6.
InterPro; IPR001149; Ribosomal_L18p.
PRINTS; PR00058; RIBOSOMALL5.
ProDom:
PR001394; Ribosomal_L18p: 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID+1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                           SEQUENCE FROM N.A.
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YIP6 OR CG17489.
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Drosophila melanogaster (Fruit fly).

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MEDLINE=ZUISOUGE; HOUNGELINGINGS.

A Manatides P.G.; Scherer S.E.; Lip Pw., Hoskins R.A., Galle R.F.;

A Manatides P.G.; Scherer S.E.; Lib Pw., Hoskins R.A., Galle R.F.;

A George R.A.; Lewis S.E.; Richards S., Ashburner M., Henderson S.N.;

Sutton G.C.; Workman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;

B strand R.C.; Rayers Y. H.G.; Blazels R.G.; Changen Pw., Prielifer B.D.;

Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Change M.; Prielifer B.D.;

A Abril J.F.; Agbayuni A., An H.-J.; Andrews-Pfannkoch C.; Baldwin D.D.;

Ballew K.M.; Basu A., Baxendle J.; Bayreakter D.; Botshakov S.;

Ballew K.M.; Basu A., Baxendle J.; Bayreakter D.; Botshakov S.;

Burtis K.C.; Busan D.A.; Buller H.; Cadieu E.; Center A.; Chandra I.,

Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.,

A Burtis K.C.; Busan D.A.; Buller H.; Cadieu E.; Center A.; Chandra I.,

Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.,

A Durbin K.J.; Evangelista C.C.; Ferriac C.; Ferriac E.; Diacks P.,

A Durbin K.J.; Evangelista C.C.; Ferriac S.; Dunkov B.C.; Dunn P.,

A Burtis K.C.; Busan D.A.; Buller H.; Galbart W.M.; Glasser K.,

Clodek A.; Gong F.; Gorrell J.H.; Gu.Z.; Gran P.; Harris M.;

A Harris N.L.; Harvey D.; Helman T.J.; Hernandez J.R.; Houck J.;

A Harris M.L.; Harvey D.; Helman T.J.; Hernandez J.R.; Houck J.;

A Liu X., Mattei B.; McIntosh T.C.; McIeod W.P.; Parle B.;

A Liu X., Mattei B.; McIntosh T.C.; McIeod W.; Parle B.;

A Bazzolo M.; Pittman G.S.; Pan B.; Pullay Y.; Lin X.;

A Reinert K.; Remidton K.A.; Bunders R.D.; Puri V.; Resse M.G.;

A Spier E.; Speanling A.C.; Stapleron M.; Skrong R.; Sun B.;

A Spier E.; Speanling A.C.; Stapleron M.; Strong R.; Sun B.;

A Reinert K.; Remidton K.; Saunders R.; Wang S.; Yao O; Zheng L.;

A Reinert K.; Remidton C.; Turner R.; Vanker B.; Wang X.; Yang S.; Yao O; Zheng L.;

A Reinert K.; Remidton K.; Saunders B.; Rang S.; Plan R.; Andrew B.; R.; Recong C.; Turner R.; Vankersen D.; Rang S.; Man S.; Pala R.; Rang S.; Pala R.; Rang S.; Pala R.; Rang S.; Pala R.; Rang S.; Pala R.; Rang
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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299 AA; 34037 MW; 523F50ED67E7841A CRC64;
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Interpro; IPR001149; Ribosomal_L18p.
                                                                                                                                                                                                                                   STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00861; Ribosomal_L18p; 1. PRINTS; PR00058; RIBOSOMALL5. ProDom; PD001394; Ribosomal_L18p;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AE002910: AAF45418.2; -.
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                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPIDDGKG 8
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A Fosler C., Gabriellan AE., Garrell J.H., Gu 2., Gabart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu 2., Gabart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Ximmel B.E., Kodira C.D., Kraft C., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
RA Merkulov G., Milshina N.V., Mobarty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Parle J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun S.,
RA Svirskas R., Tector C., Turner R., Verler E., Wang A.H., Wang X.,
RA WINSTON M., Weisschock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weisstor G.M., Weisstor G.M
                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holt R.A., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Burndon R.C., Rogers Y. H.C., Blazej K.G., Champe M., Pfelifer B.D.,
Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
And K.H., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Abrits K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A Durbin K.J., Evangelista C.C., Ferriaz S., Pleischmann W.,
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Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfelffer B., Poon L., Sequaira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M.. Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
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MEDLINE-99403001: PubMed-10471707;
MEDLINE-99403001: PubMed-10471707;
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.:
                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker S., Rubin G.M.: "An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AE003646; AAF53435.1; -.
EMBL; AE003412; AAF44915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics 153:179-219(1999).
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                                                                                                                                                                                  SECUENCE FROM N.A.
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                                                                                         Ephydroidea; Dro
NCBI_TaxID-7227;
                                                                                                                                                                                                                     STRAIN-BERKELEY;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Arabidopsis thaliana BAC 726F17 from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecker J.R.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2167 AA; 250307 MW; 3C57E34ADDD89A42 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last aunotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROG035; MYOSITHEAVY.
PRODOM; PRO0035; MYOSITHEAVY.
PRODOM; PRO0035; MASIN_head; 1.
SMART; SM0015; 10; 3.
SMART; SM0015; 10; 3.
SMART; SM00139; MYTH4; 2.
SMART; SM00136; MYH4; 1.
PROSITE; PS50005; 10; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
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                                                                                        InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
InterPro; IPR000857; MyTH4.
InterPro; IPR000567; SBP_bac_l.
InterPro; IPR001452; SH3_
                         FlyBase; FBgn0000317; ck.
InterPro; IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                      Pfam; PF00612; IQ; 4.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00784; MyTH4; 2.
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                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00018; SH3;
HSSP; P08799; 1MND
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SEQUENCE FROM N.A.
STAIN-ATCC 10089 / CB15;
MEDLINE_21173699; Dubmed-11259647;
MEDLINE_21173699; Dubmed-11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson W.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., PhadRe N.D., Ely B.,
DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                            SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brocks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kinn C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lea S., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Pelm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC013482; AAF16542.1;
InterProc IPRO00620; DUF6.
Fram: PF00892: DUF6.
Pfam: PF00892: DUF6.
Pfam: PF00892: DUF6.
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                                                                                                                                                                                                                                                                                                                          75.5%; Score 37; DB 10; Length 391; 66.7%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS00331; MALIC_ENZYMES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00515; BPD_transp.
InterPro; IPR01891; Malic_enzyme.
InterPro; IPR002505; PTA_PTB.
Pfam; PF00390; malic; 1.
Pfam; PF01515; PTA_PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADP-DEPENDENT MALIC ENZYME.
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       359 KPVDTGKGL 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                    1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       759 OPVDDGEG 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caulobacter
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9A2L2;
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Q9A2L2
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COSMID 5B8
                              Query Match
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                                                                                                                                                                                                                                                                                   RESULT 12
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                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy 'Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Burloy 'Hubler F., Barnett M.J., Cadleu E., Capela D., Chain P., Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Golduck S., Godrie T., Goffeau A., Goldung B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Kann M.L., Kalman C., Peck M.C., Pohl T.W., Portetalle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Vorhoelter F.J. Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.; Science 293:668-672(2011).
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STRAIN-ATCC 15692 / PAO1:

MEDIUB-20437337; bubMed-10984043;

MEDIUB-20437337; bubMed-10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbock-Wadman S., Yuan Y., Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Sencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLRel. 19, Last annotation update)
PROBABLE N-ACETYLMURAMOYI.-L-AIANINE AMIDASE AMIC PRECURSOR
TRANSMEMBRANE PROTEIN (EG. 3.5.1.28).
Rhizoblum meliluti (Sinorhizoblum meliloti).
Rhizoblaceae: Sinorhizoblum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.5%; Score 36; DB 16; Length 410; Best Local Similarity 62.5%; Pred. No. 1.3e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE004763, AAG06809.1, -
Hypothetical protein, Complete proteome.
SEQUENCE 456 AA, 50690 MW, BFE2F230EC94F736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Complete protecme.
SEQUENCE 410 AA; 44588 MW; CF55FC972194EB8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PA3421.
                                                       410 AA.
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                                                       PRT;
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STRAIN=1021;
MEDLINE=21368234; Pubmed=11474104;
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Nature 406:959-964(2000).
                                                       PRELIMINARY;
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                                                                                  Q926D3;
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                                                    Q926D3
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, ALO22374; CAA18516.1;
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID*1902;
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73.5%; Score 36; DB 16; Length 456; 66.7%; Pred. No. 1.5e+02;
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                                                1; Indels
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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19, Last annotation update)
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Last annotation update)
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                                                2; Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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InterPro; IPR001687; ATP_GTP_A.
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MEDLINE=97000351; PubMed=8843436;
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                                                6; Conservative
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                         Best Local Similarity
                                                                                                                         SEQUENCE FROM N.A.
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                                                                                             1 EPIDDGKGL 9
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SEQUENCE FROM N.A.

STRAIN+ATCC 15692 / PAO1;

MEDLINE-20437337; bubMed=10984043;

MEDLINE-20437337; bubMed=10984043;

Stover C.K., Pham x.-O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A. Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Claus H., Stoevesandt J., Frosch M., Vogel U.; "Genetic isolation of meningococci of the electrophoretic type 37
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                                                                                                                                                                                                                                                                                                    73.5%; Score 36; DB 9; Length 1421; 75.0%; Pred. No. 5.2e+02; ative 1; Mismatches 1; Indels
                                                                                      J. Bacteriol. 183:2570-2575(2001).

EMBL; AJ278707; CAC19023.1; -.
InterPro: IPR003961; FN_III.
SMART; SMO0605; FN3; I.
SEQUENCE 1421 AA; 153413 MW; 7A17FD4AEB6FA9A6 CRC64;
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InterPro: IPR001899; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 5627 AA; 573167 MW; 2D2A1154C99D3750 CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA2462.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Virusus: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                          Query Match 73.5%
Best Local Similarity 75.0%
Matches 6; Conservative
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317 EPVDDGFG 324
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NCBI_TaxID=287;
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A MADLINES, 7440470; PUDMECH9201388;
A MADLINES, 7440470; PUDMECH9201388;
A Vasudevachari M.B., Salzman N.P.;
A Vasudevachari M.B., Salzman N.P.;
A Vasudevachari M.B., Salzman N.P.;
The professe gene and in its Gag substrate cleavage sites.";
J. Virol. 71:6662-6670(1997).
R RASP, POSSB8; JAAR.
InterPro: IPRO01878; Znf_CCHC.
R RASP, PRO098; Zf_CCHC.
R RASP, PRO098; Zf_CCHC.
R RANAT; SM00343; Znf_CZHC; Z.
R RANAT; SM00343; Znf_CZHC; Z.
R NATITS, PRO0989; Znf_CZHC; Z.
R SMART; SM00343; Znf_CZHC; Z.
R SMART; SM00343; Znf_CZHC; Z.
R SWART; SM00343; Znf_CZHC; Z.
R SWART; SM00343; Znf_CZHC; Z.
R SWART; SM003478; Znf_CZHC; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                           STRAIN=PATIENT 5;
MEDLINE=97404676; PubMed-9261388;
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A. SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:
SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:
SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:
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7.215 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1991.DAT:*
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Human PRO1025
                                                                                                                                               August 6, 2002, 16:52:53 ; Search Lime 138.55 Seconds
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GenCure version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                      US-10-020-139-2_COPY_115_123
                                                                                                       M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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N-PSDB; AAV44759
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New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening

Claim 16; Fig 1; 94pp; English.

This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding special correcome identification of the corresponding of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pencreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antipacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, polypeptides and antisense nucleic express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.

249 AA;

; 0 0; Gaps 100.0%; Score 49; DB 19; Length 249; 100.0%; Pred. No. 0.084; Live 0; Mismatches 0; Indels ( lery Match
local Similarity 100.
fatches 9; Conservative

1 EPIDDGKGL 9

3ULT 460682

AAW60682 standard; Protein; 249 AA.

AAW60682;

18-SEP-1998 (first entry)

Human parotid secretory protein (HPSP).

secretory tissue; gastrointestinal tissue; HPSP, Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis. Parotid secretory protein; human; cancer; autoimmune disease;

Homo sapiens.

22-MAY-1998.

97WO-US20651. 07-NOV-1997; 96US-0749288. 14-NOV-1996;

(INCY-) INCYTE PHARM INC.

Goli SK;

Bandman O,

WPI; 1998-297933/26.

N-PSDB; AAV37699.

New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or

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antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP may sources. Expression of HPSP may indicate cell proliferation HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease,
                                                                  This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HSPs are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, protate, breast, gastrointestinal tract or panetreas, Slorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, paneratitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HSPS nucleic acid are used to produce recombinant HSSP which is used to generate antibodies and screen for its antagonists. Antibodies are useful directly as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                    but also for mapping the chromosomal sequence.
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                                   Claim 1; Fig 1A-C; 65pp; English.
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gastrointestinal tissues
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 249 AA;
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07-JUL-1999;
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99US-0141032.

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25-JUN-1999;
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                                                                                                                                                                                                                                                                                          The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0390, PR0311, PR0335, PR0619, PR0717, PR06199, PR0848, PR0848, PR0943, PR01005, PR01009, PR01025, PR01030, PR01097, PR01111, PR01131, PR01181, PR0
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                                                                                                                                              Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 49; DB 21; Length 249; ilarity 100.0%; Pred. No. 0.084; Conservative 0; Mismatches
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                                                                                                                                                                                                                                       Claim 61; Fig 26; 286pp; English.
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Watanabe CK, Wood WI;
                                                            WPI: 2000-572270/53.
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                                                                                        N-PSDB; AAC58379
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may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheiner's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87725-A8774 which encode human secreted proteins AAB87563-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the converse and a purified antibody capable of binding to one of the sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are method for storing the sequence data on a computer system, and a method for storing the sequence data on a computer system, and a method for storing features of the cOMA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins of fragments to obtain antibodies capable of specifically binding to the secreted proteins. The CDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention
                                                                                                                                                                                     Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
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Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                              Claim 9; Figure 10; 306pp; English.
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99US-0469099.
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Best Local Similarity 100.v
9; Conservative
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                                                                                                                                                                                                                                                                        mapping procedures -
                                                                          WPI; 2000-442637/38.
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                                                                                                               N-PSDB; AAA87727
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mutinifiammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-muticide; anti-muticide; anti-muticide; antiantence; cardialer; antialerary; antiulcer; osteopathic; cacema; dermatological; antialergic; antiasthmatic; antidiabetic; oytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatological arthritis; septic shock; pancratitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; entrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer; diabetes; multiple sclerosis; depression; Alzheimer; disoase; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                          0; Indels 0; Gaps
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                                                                      49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples \cdot
                                                                                                                                                                The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 49; DB 22; Length 249; Best Local Similarity 100.0%; Pred. No. 0.084; Matches 9; Conservative 0; Mismatches 0; Indels (
Dumas Milne Edwards J, Bouqueleret L, Jobert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:1260.
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                                                                                                                                Claim 10; Page 281; 307pp; English.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                    WPI; 2001-071487/08.
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                                                                                                                                                                                                                                                                 249 AA;
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                                                                                                                                                                                                                                                                 Sequence
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AAM25745
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AAM25965. The proteins can have activities based on the tissues and calls they are expressed in, such as: antiinflammatory; antiinflammatic; calls they are expressed in, such as: antiinflammatic; antiarthritis they are expressed in, such as: antiinflammatic; calls they are expressed in, such as: antiinflammatic; antiarthritis; immunosuppressive; antibacterial; endocrine; cardiant; cardianaemic; antiagregant; haemostatic; unnerary; cardiadvascular; antianaemic; antidiabetic; cytostatic; neuroprotective; antidiabetic; cytostatic; neuroprotective; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidiaterin; then can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for appoints or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatiiis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, anemaia, platelet disorders, thrombooytopaenia, wounds, burns, uleers, difficities and proprosis; contents and proprosis and antipolicities antipolicities and antipolicities and antipolicities and antipolicities and antipolicities and antipolicities antipolicities antipolicities antipolicities antipolicities antipolicities antipol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
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                         Claim 20; Page 260; 1217pp; English.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders.
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Best Local Similarity
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            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more yenes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                     Gaps
                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                            Score 38; DB 22; Length 299;
Pred. No. 17;
1; Mismatches 1; Indels
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75.0%;
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                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                        (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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|133 epvddgpg 140
                                                                                                                                                                                                                                                                                                                             1 EPIDDGKG 8
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB67420;
                                                                                                                                                                                                                                                                                        Matches
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                           0
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                                                       77.6%; Score 38; DB 22; Length 299; 75.0%; Pred. No. 17;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.6%; Score 38; DB 22; Length 2167; 85.7%; Pred. No. 1.6e+02; tive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ 1D NO 7899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD, Myers EW;
                                                                                                                                                                                                                ABB60369 standard; Protein; 2167 AA.
                                      Query Match
Best Local Similarity 75.05,
150 6: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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Best Local Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
               299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
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                                                                                                                                         133 epvddgpg 140
                                                                                                               1 EPIDDGKG 8
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                                                                                                                                                                                                                                                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions -
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             Sequence
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #29544.

18-FEB-2002 (first entry)

ABG29553;

ABG29553 standard; Protein; 127 AA.

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ABG29553
RESULT
                                                                                 The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 54862; 103pp; English.
                                                                                                                                                                               Novel human diagnostic protein #24494.
                                                           ABG24503 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                            18-FEB-2002 (first entry)
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Best Local Similarity 66./۳
احداد 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA;
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                                                                                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
                                                                                                    ABG24503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                            ABG24503
                         RESULT
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Tang YT;

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

WO200175067-A2. Homo sapiens.

1-0CT-2001.

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The invention relates to isolated polynucleotide (1) and probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome conjunction and pane mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in tracting disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 59912; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Drmanac RT, Liu C,
                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 127 AA;
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67 eviddgrgm 75
                                                                                                                                N-PSDB; AAS93740.
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Gaps

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.71.4%; Score 35; DB 22; Length 98; 66.7%; Pred. No. 19; 1; Indels

| ||||:|: 60 eviddgrgm 74

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1 EPIDDGKGL 9

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AAU57477 standard; Protein; 414 AA.
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                               RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence comprises one of 98 enzymes of the everninomicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 296;
                                                                                                                                                                                                                                                                                                                                                                        Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                                                                                                                                                       Micromonospora everninomicin biosynthetic enzyme ORF3.
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71.4%; Pred. No. 68;
Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micromonospora carbonacea var. africana
                                        AAU04903 standard; Protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 12; 109pp; English.
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Best Local Similarity 71.48
Matches 5; Conservative
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442147/47.
                                                                                                                                                                                                                                                                                                                                                                                                                     termentation; ORF3.
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                                                                                                                                                                                                          26-SEP-2001
AAU04903
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by be across. The disorders include SARHO syndrome (synovitis, acros, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Process is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P. across in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     SAPHO syndrome: synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang SS, Bhatia A;
                                                                     Propionibacterium acnes immunoyenic protein #18373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham JL, Wany ... 
Carter D;
                                                                                                                                                                                                                                                               dermatological; osteopathic; neuroprotectant.
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13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Persing DH,
                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes.
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Matches 5; Conserv
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polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques (II). (II) is useful for qenerating antibodies against it, detecting or quantitating a polypeptide in Lissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imaging of sites expressing (11). (1) and (11) are inserted in detail of stress involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010.ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 35; DB 22; Length 481; 66.7%; Pred. No. 1.2e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 59914; 103pp; English.
                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #29546.
                                                                             ABG29555 standard; Protein; 481 AA.
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N-PSDB; AAS93742.
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                                                                                                                                                          ABG29555;
RESULT 14
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic the treatment, prevention and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. A caces is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of p. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and downregulate expression and activity of P. acnes polypeptides and activity of P. acnes proteins acrea accordance accord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                           SAPHO syndrome; synovilis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang SS, Bhatia A;
                                                                                                                                                                       Propionibacterium acnes immunogenic protein #1916.
                                                                                                                                                                                                                                                                                                                Jermatological; osteopathic; neuroprotectant.
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e J, Zhang Y, Jen S, Carter D;
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AAU41020 standard; Protein; 511 AA.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                (first entry)
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Search completed: August 6, 2002, 16:52:54 Job time: 336 sec

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                                                        August 6, 2002, 16:53:55; Search time 51.22 Seconds
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
    /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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US-08-282-197C-55
US-08-687-865A-2
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                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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US-09-377-155-32
US-08-913-942-2
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US-08-718-905-3
US-09-550-497-3
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US-09-268-347-44
US-09-396-651B-1
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Listing first 45 summaries
                                     OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FILING DATE: 29-DEC-1995
                                                                                                                                                                  US-09-199-637A-331
US-07-779-172A-3
US-08-106-433A-2
US-08-480-604A-28
                                US-09-046-086-2
US-08-480-604A-23
US-08-405-496A-23
US-08-915-136-23
US-08-915-136-23
US-08-4915-136-26
US-08-245-294-8
US-08-245-294-8
US-08-307-279A-8
PCT-US95-06211-8
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 US-08-476-254-10
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Van Solingen, Pieter
APPLICANT: Williams, Diane P.
APPLICANT: Farrell, Roberta L.
APPLICANT: Farrell, Roberta L.
APPLICANT: Herbes, Wilhelmina T.
APPLICANT: Herbes, Wilhelmina T.
APPLICANT: Van Der Kleij, Wilhelmus A.
APPLICANT: Van Beckhoven W.C., Rudolf F.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Ones, Brian E.
TILLE OF INVENTION: ALKALI-TOLERANT XYLANAS.
                                                                                                                                                                                                                                          ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 425
ATORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFRERENCE/DOCKET NUMBER: 4615-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-150
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08501126
; Patent No. 6140095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
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US-08-501-126-2
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USA
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US-08-501-126-2
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67.3%; Score 33; DB 4; Length 396;

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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Kevin F.
APPLICANT: Jones, Kevin F.
APPLICANT: Zagursky, Robert J.
APPLICANT: Ool, Peggy
TITLE OF INVENTION: The NucA Protein of Haemophilus
TITLE OF INVENTION: Influenzae and the Gene Encoding That Protein
NUMBER OF SEQUENCES: 23
CORRESPEDING ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                             APPLICANT: Brzezinski, Hyszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 33; DB 2; Length 397;
77.8%; Pred. No. 93;
tive 0; Mismatches 2; Indels
             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
      Pred. No. 93;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29.JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                ; Sequence 55, Application US/08282197C; Patent No. 5871730; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08687865A
; Patent No. 5955596
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATOCKNEY/AGENT INFORMATION:
NAME: Cimbal a. Michale A
REGISTRATION NUMBER: 33.851
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 397 amino acids
amino acid
Best Local Similarity 77.8 Matches 7; Conservative
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Best Local Similarity 77.0.
                                                                                           195 EVIDDGGGL 203
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195 EVIDDGGGL 203
                                                                  1 EPIDDGKGL 9
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                                                                                                                                                                         RESULT 2
US-08-282-197C-55
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US-08-282-197C-55
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US-08-687-865A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Sequence 2, Application US/09043711
Patent No. 6221365
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Zagursky, Robert J.
APPLICANT: Zagursky, Robert J.
APPLICANT: Ool, Peggy
TITLE OF INVENTION: The NucA Protein of Haemophilus
TITLE OF INVENTION: Influencae and the Gene Encoding That Protein
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
67.3%; Score 33; DB 2; Length 603;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-IXOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,865A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,711
                                                                                                                                               26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/687,865
TILING DATE: 26-01U-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DGOKET NUMBER: 33,250-00
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                             NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 33,2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 603 amino acids TYPE: amino acid mobloGY: linear.
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
New Jersey
U.S.A.
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: U.S.A.
                                                                                                                                                                                                    FILING DATE: 26 CLASSIFICATION:
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                                     07470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-687-865A-2
                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-043-711-2
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APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              67.3%; Score 33; DB 4; Length 603; 85.7%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 65.3%; Score 32; DB 1; Length 58; Best Local Similarity 71.4%; Pred. No. 19; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Trask, Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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Sequence 15, Application US/08470179

Patent No. 5645994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Borrelia burgdorferi
US-08-470-179-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sweigert Ph.D. Susan E. REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-532-1922
TELEFAX: 801-531-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                  : LENGTH: 603 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-043-711-2
                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 58 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 801-531-9108
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 84110
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                      525 EPIDDNK 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Utah
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51 IDDGRGI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IDDGKGL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: S
STATE:
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Gaps
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Donovan, Judith C.
Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
COMPOSITIONS AND USES THEREFOR
                                                                                   APPLICANT: Donovan, William P.
APPLICANT: Donovan, Judith C.
APPLICANT: Donovan, Judith C.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 65.3%; Score 32; DB 3; Length 267; Best Local Similarity 71.4%; Pred. No. 95; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: CONCULTENTLY HENCEMITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                   Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DCKET NUMBER: MOBT:003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                       : Sequence 3, Application US/08718905
; Patent No. 6063756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09550497
Patent No. 6248536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-718-905-3
                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                     ADDAL
STREET: F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CC CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PLDDNKG 241
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US-08-718-905-3
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. Sequence 9, Application US/09323427
. Patent No. 6248329
                               US-09-323-427-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34 TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.3%; Score 32; DB 4; Length 267;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/550,497
FILING DATE: 14-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                     PRIOR CAPALICATION DATA:

APPLICATION NUMBER: 08/718,905
FILING DATE: AUNROWN>
ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: MOBT:003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING JUAL:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,905
FILING DATE: 24-5EP-196
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/147,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 267 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09147992; Patent No. 6326331; GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 71.4<sup>§</sup>
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single;
TOPOLOGY: linear
US-09-147-992-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
'...s 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 PLDDNKG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-550-497-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-147-992-3
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23t PLDDNKG 241

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GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasilic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
TITLE OF INVENTION: Molecules, and Uses Thereof
TITLE OF INVENTION: Molecules, and Uses Thereof
CURRENT APPLICATION UNBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION UNBER: 60/087,435
EARLIER PILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6171789el Insertion Sequence from a Virulent ent No. 6171789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

65.3%; Score 32; DB 4; Length 419;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/011,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/002,398
FILING DATE: 17-AUG-1995
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . UMGANISM: Burkholderia cepacia
; INDIVIDUAL ISOLATE: ET12/cblA
US-09-011-197-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-011-197-4
; Sequence 4, Application US/09011197
; Patent No. 6171789
                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Dirofilaria immitis
US-09-323-427-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 VDDGKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IDDGKG 8
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 9
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US-08-913-942-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%; Score 32; DB 1; Length 658;
66.7%; Pred. No. 2.5e+02;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                       E: Flehr, Hobbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
ITILE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                 APPLICANT: Barenkamp, Stephen 1.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: S11va, RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 4-61053/RFT
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/409,995
24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      Sequence 5, Application US/08409995; Patent No. 5646259; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-685-467-5
; Sequence 5, Application US/08685467
; Patent No. 6060059
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   658 amino acids
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Matches 6; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                STREET: Four contraction
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FILING DATE: 24-MAR
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                       94111-4187
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                          10 PVEPGKGL 17
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2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                       US-08-409-995-5
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24 WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: VANCE, DOLLY A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RWS/DAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08913942
Patent No. 6200578
GENERAL INFORMATION:
APPLICANT: St. Gene, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/685,467 FILING DATE: US/101-1996 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942 FILING DATE: 29-DEC-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                            A-61053-2/RFT/RMS
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US U8/409,995
FILING DATE: 24-WAR-1995
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             NAME: SILVA, RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5.
SEQUENCE CHARACTERISTICS:
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ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-685-467-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
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350 EDADEGKGL 358
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                                                                                                                                                                                                                                                                                                        65.3%; Score 32; DB 4; Length 658; 66.7%; Pred. No. 2.5e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Flehr, Hobbach, Test, Albritton & Herbert
: Four Embarcadero Center, Suite 3400
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
CORRESPONDENCE: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNBER: 34,304
REFERENCE/COCKET NUMBER: 34,304
REFERENCE/COCKET NUMBER: 34,304
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (415,398-3249
ITELEX: 910 272599
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/409,995
24-MAR-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEAX: (415) 388-3249
TELEX: 910 277299
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 2, Application US/08409995
; Patent No. 5646259
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.79
Matches 6; Conservative
                                                                                                                                                                                unknown
                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-913-942-5
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unknown
                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-409-995-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-409-995-2
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350 EDADEGKGL 358

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1 EPIDDGKGL 9

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0; Gaps
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                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                              APPLICANT: St. Geme III, Joseph W.
PPLICANT: Barenkamp, Stephen J.
APLICANT: Barenkamp, Harmophilus Adhesion PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-61053-2/RFT/RMS
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Job time: 288 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                Sequence 2, Application US/08685467
Patent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-(TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Silva, Robin M. REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-685-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415, 781-1989)
TELEFAX: (415, 398-3249)
TELEX: 910, 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
                                                                                                                                                                                                                                                                            COUNTRY: United States 21P: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                         STREET: Four concepts
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 EDADEGKGL 358
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US-08-685-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 7, 2002, 06:43:38; Search time 14.84 Seconds (without alignments) 51.800 Million cell updates/sec Run on:

US-10-020-139-2\_COPY\_159\_166

1 ЕТБРОТИО 8 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Scor	Query		1		
	Match	Length	P	10	Description
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ν,	1.9/	Ω	7	T48145	probable transcrip
3	76.1	$\sim$	~	C82564	
e	76,1	4	7	T01782	GDP dissociation i
٣	76.1	m	~	S76525	ionine-
m	76.1	4	7	G86573	DNA polymerase 111
9	76.1	24	N	B72050	
m	73.9	4	~	T10801	
m	73.9	7	Н	A30882	; ;
m	73.9	674	7	149479	1 7
m	73.9	C	~	T17345	1 0
c	71.7	85	-	BVECNP	tatio
m	71.7	92	?	F85982	
m	71.7	~	7	AD1009	
33	71.7	321	7	T08462	hypothetical prote
m	71.7	æ	7	T10898	probable omega-3 f
0 33	71.7	$\sim$	N	C98200	Serine hydroxymeth
m		$\sim$	~	AF3086	
m	ä	2	7	G72037	>
m	71.7	2	~	B86586	- С
m	71.7	$\sim$	~	T46107	hypothetical prote
m	71.7	~	~	H84773	
3	71.7	490	7	B75538	IDP-N-acetylairano
m	71.7	0	7	833761	transferrin precur
m	71.7	9	~	T12678	3
m	71.7	C	7	C69048	ji

RESULT T02030

Σ

GDP dissociation inhibitor protein - rice
C:Species: Oryza sativa (rice)
C:Species: Oryza sativa
C:Sp

hypothetical prote	hypothetical prote	_	hypothetical prote		myb-related protei	myb-related protei	myb-related protei	myb-related protei	hypothetical prote	asparaginetRNA l	hypothetical prote	choline dehydrogen	probable atsF prot		S
097991	F75400	T31239	T08326	D85096	T02984	868688	JQ0957	T09879	T19149	E70112	S75491	AC0143	F70651	C43674	S15727
:1	?	~	7	7	?	-	٦	7	7	7	a	C)	.7	~	7
109	146	207	233	236	239	249	274	294	416	466	522	267	603	669	739
9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69
~	3.2	32	3.2	32	32	32	32	35	32	32	32	32	32	32	32

# ALIGNMENTS

RESULT
AI3321
5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5) [imported] - Brucella me]iter
C;Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text change 15-Feb-2002
C; Accession: AI3321
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivano
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Haqius, S.; O'Callaghan, D.; Le
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intrace) ular pathogen Brucella mel
A; Reference number: AD3252; PMID:11756688
A;Accession: AI3321
A:Status: preliminary
A; Molecule type: DNA
A:Residues: 1-274 <kur></kur>
A; Cross-references: GB; AE008917; P1DN; AAL51740,1; P1D; a17982477; GSPDB; GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME10559
A; Map position: I
C;Superfamily: 5,10-methylenetetrahydrofolate reductase (FADH2)
C;Keywords: oxidoreductase
Pred. 'No.
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Фу 1 Епоротно в
Db 214 DNDPQTHQ 221

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Cipacies: Xylella fastidiosa
Cipacies: Xylella fastidiosa
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Cipacession: C82564
Rianonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Se Aittle: The genome sequence of the plant pathogen Xylella fastidiosa.
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                                                                     R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                            A;Wolecule type: DNA
A;Residues: 1-250 <HEV/>A;Residues: 1-250 <HEV/>A;Cross-reterences: EMBL:AL080318
A;Experimental source: cultivar Columbia; BAC clone T4C9
C;Genetics:
A;Map position: 4
A:Introns: 2,22; 52/2
A;Note: T4C9.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.1%; Score 35; DB 75.0%; Pred. No. 24;
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Pred. No. 42;
0; Mismatches
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85.7%;
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Matches 6; Conservative
                                                                                                                                                                      A;Reference number: 224485
A;Accession: T48145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 EIDPSTHO 91
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71 TDPYTHQ 77
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C82564
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(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Academic 10423
(Species: T0423
(Species: T0423
(Species: Protein Sequence Database, February 1999
(Species: Arabidopsis T15376
(Species: T15376
(Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Oryza sativa (rice)
C:Accession: T0202
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Kim, C.Y.: Cheon, S.Y.: Jeong, S.Y.: Cheong, Y.H.; Choe, M.S.; Park, H.C.: Cho, M.J.
R:Reference number: Z14502
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1.445 < KIM>
A:Residues: 1.445 < 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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;
                                                80.4%; Score 37; DB 2; Length 445; 75.0%; Pred. No. 18; 1; Indels 1; Mismatches 1; Indels
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87.5%; Pred. No. 59;
                                                                                                                                                           1; Indels
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Query Match
Best Local Similarity 75,00
Feet Conservative
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                 151 EADPKTHQ 158
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                                                                                                                                                                                                                                                 1 ETDPOTHO 8
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Gaps

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A.Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hici, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzl Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydla pneumoniae AR A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase III, alpha chain CP0081 [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: B72050; E81616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood Nature Genet. 21, 385-389, 1999
A;Tilte: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Reference number: B72050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: DNA
A.Residues: 1-1240 (REA>
A.Cross-references: GB:AE002171; GB:AE002161; NID:97189009; PIDN:AAF37967.1; PID:97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1240 cARN>
A;Cross-references: GB:AF001549; GB:AE001363; NID:g4376963; PIDN:AAD18805.1; PID:g4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Accession: T10801
R.Beyser, K.: Fabry, S.
submitted to the EMBL Data Library, July 1996
A.Description: Identification and characterization of a lower plant Ypt/Rab guanosi
A.Reference number: 217156
A.Accession: T10801
A.Status: preliminary: translated from GB/EMBL/DDBJ
                     A;Cross-references: GB:BA000008; NID:g8979038; PIDN:BAA98873.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDP dissociation inhibitor GDI1 - Volvox carteri f. nagariensis
C;Species: Volvox carteri f. nagariensis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                         76.1%; Score 35; DB 2; Length 1240; 75.0%; Pred. No. 1.3e+02; Live 0; Mismatches 2; Indels
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A;Residues: 1-443 - ABEX>
A;Cross-references: EMBL:U62866; NID:91572517; PID:91572518
A;Experimental source: strain HK10
                                                                                                                                                          C;Superfamily: DNA-directed DNA polymerase Ill alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: dnaE; CP0081
C;Superfamily: DNA-directed DNA polymerase III alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                        Best Local Similarity 75.0 Matches 6; Conservative
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Best Local Similarity
5, Conserva
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                                                                                                                              A; Gene: dnaE
                                                                                              C; Genetics:
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A;Molecule type: DNA
A;Residues: 1-532 <KAN>
A;Residues: 1-532 <KAN>
A;Cres-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10371.1; PID:g100164
A;Cres: the nucleotide sequence was submitted to the EMBI, Data Library, June 1996
C;Superfamily: methionine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rishirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
ArTitle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DAR Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Synechocystis sp.
Ayariety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C:Accession: S76525
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 26-May-2000
C;Accession: T01782
R;Ezaki, B.; Koyanaqi, M.; Gardner, R.C.: Marsumoto u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methionine--tRNA ligase (EC 6.1.1.10) · Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
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                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: GDI
C,Function:
A;Description: inhibits dissociation of GDP from GTP binding proteins
C,Superfamily: human GDP dissociation inhibitor XAP-4
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O
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                                          Chacession: T01782
R:Ezaki, B.; Koyanagi, M.; Gardner, R.C.; Matsumoto, H.
submitted to the EMBL Data Library, July 1997
A; Reference number: Z14424
A; Reference number: Z14424
A; Accession: T01782
A; Status; preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Residues: 1-444 < EZAA
A; Cross-references: EMBL.AF012823; NID:92501849; PID:92501850
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                                                                                                                                                                                                                                                                                                                                                A; Experimental source: cultivar Samsun C; Genetics:
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Best Local Similarity 85.78
Matches 6; Conservative
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Best Local Similarity 62.5%
Matches 5; Conservative
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A.Molecule type: DNA
A.Residues: 1-1240 <STO>
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Gaps

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C.Species: Homo sapiens (man)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A,Residues: 1-1223 <DUE>
A,Cross-references: EMBL:AL117665
                                                                                                                                                                                                                                                                                                                                                                                             73.9%;
75.0%;
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Best Local Similarity 75.00
Best Local 6; Conservative
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Best Local Similarity 83.3.
The 5; Conservative
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A; Residues: 1-92 < BLAT>
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1040 ETDPETSQ 1047
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A;Molecule type: DNA
A;Residues: 1-92 <CHO>
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                                                   C; Accession: T17345
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                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Rattus norvegicus (Norway rat)
C; Date: 10. Sep-1999
C; Accession: A3082
C; Accession: A3082
R; Balcarek, J.M.; Theisen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, M. Balcarek, J.M.; Theisen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, M. A; Title: Icolation and characterization of a cDNA clone encoding rat 5-lipoxygenase. A; Reference number: A30882
A; Accession: A30882
A; Accession: A30882
A; Molecule type: MRNA
A; Residues: 1-670 c8AL>
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C. A.: Kurre, U.: Jenkius, N.A.: Copeland, N.C.: Funk, C.D.
J. Biol. Chem. 270, 17993-17999, 1995
A. Fitte: CDNA cloning, expression, mutagenesis, intracellular localization, and gene chr. A. Accession: 149479
A. Accession: 149479
A. Status: preliminary: translated from GB/EMBL/DDBJ
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C;Species: Mus musculus (house mouse)
C;Date: 02-jul-1996 #sequence_revision 02-jul-1996 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                       Gaps
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A;Residues: 1-674 <RES>
A;Cross-references: GB:L42198: NID:g886332; PIDN:AAC37673.1; PID:g886333
C;Genetics:
A;Gene: Alox5
C;Superfamily: arachidonate 5-lipoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J03960; NID:9205228; PIDN:AAA41538.1; PID:9205229 C;Superfamily: arachidonate 5-lipoxygenase
                       A;Description: Inhibits dissociation of GDP from GTP binding proteins C;Superfamily; human GDP dissociation inhibitor XAP-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.9%; Score 34; DB 1; Length 670; 75.0%; Pred. No. 1.1e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.9%; Score 34; DB 2; Length 674; 75.0%; Pred. No. 1.1e+02; tive 1; Mismatches 1: Indels
                                                                                                                      73.9%; Score 34; DB 2; Length 443; 62.5%; Pred. No. 68;
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein DKF2p586M1824.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                        arachidonate 5-lipoxygenase (EC 1.13.11.34) - rat
                                                                                                                                                                     3; Mismatches
                                                                                          Ouery Match
Best Local Similarity 62...
5. Conservative
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Best Local Similarity 75.uv
Best Local 6, Conservative
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Best Local Similarity 75.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                               151 ESDPKTHK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 KTDPCTHQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 KTDPCTHQ 304
                                                                                                                                                                                                                   1 ETDPQTHQ 8
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C; Function:
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Across-references: GB:x68873; NID:g42128; PIDN:CAA48736.1; PID:g42129
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Tile: The complete genome sequence of Escherichia coli K-12.
A;File: The complete genome sequence of Escherichia coli K-12.
A;Accession: F65109
A;Accession: F65109
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AF000399; GB:U00096; NID:g2367201; PIDN:AAC76220.1; PID:g1786
A;Experimental source: strain K-12, substrain MG1655
C;Comment: This protein is involved in positive regulation of the metabolism of suga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Choi, Y.L.; Nishida, T.: Kawamukal, M.; Utsumi, R.; Sakai, H.; Komano, T. J. Bacteriol, 171, $222-5255, 1989
A;Fitle: Cloning and sequencing of an Escherichia coli gene, nlp, highly homologous A;Reference number: JV0027; MJID:89359178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugar fermentation stimulation protein B (NER-like protein) - Escherichia coli N.Alternate names: ner-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 27-Nov-2001
C;Accession: JV0027; F65109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Ribuesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A:Reference number: 218727
A:Accession: T17345
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 33; DB 1; Length 92; 83.3%; Pred. No. 20; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             A;Experimental source: adult uterus; clone DKF2p586M1824 C;Genetics:
A;Note: DKF2p586M1824.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: nlp
A.Map position: 69 min
G.Superfamily: phage D108 DNA-binding protein
C.Keywords: DNA binding; transcription regulation
F:50-68/Region: DNA binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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CenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 7, 2002, 06:44:08; Search time 10.33 Seconds
(without alignments)
29,986 Million cell updates/sec
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Title: US-10-020-139-2\_COPY\_159\_166

Perfect score: 46
Sequence: 1 ETDPQTHQ 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 1052
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Maximum Match 038
Post-processing: Minimum Match 1008
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		chlamy	homo sapie	mesoci	P12527 rattus norv				deino			meiot	O51128 borrelia bu		emerice	herpes	clost	homo	рошо		Б		Ψ.	$\sigma$	10	_			bacillus o	sus scro	camelus	dans cap	O66880 aquifex aeo
SUMMARIES	ΙD	λ	DP3A_CHLPN	FXY5_HUMAN	LOX5_MESAU	LOX5_RAT	LOX5_MOUSE	SPSB_ECOLI	FD3E_PHAAU	MURE_DEIRA	TRFE_HORSE	ACFX_HUMAN	PROB_MEIRU	SYN_BORBU	- 1	SCOB_EMENI	VGLG_HSV2H	GUNF_CLOTM	TAC3_HUMAN	HBP1_HUMAN	YRPA_SYNPY		KSGD_ARATH	INTA_ECOLI	CRTC_DICDI	KSGT_ARATH	AIRE_HUMAN		CDGT_BACS2	m,	ICA_PIG		HS9A_HORSE	DNLJ_AQUAE
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	Score	m	35	34	34	34	34	33	33	33	33	33	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
	Result No.		5	3	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	. 26	27	28	29	30	31	32	33

P08238 homo sapien	P11499 mus musculu O57521 brachydanio	Q04619 gallus gall	090474 brachydanio	P11501 gallus gall	P07900 homo sapien	P46633 cricetulus	P07901 mus musculu	002705 sus scrofa	Q9y5e3 homo sapien	Q59119 aeromonas h
HS9B_HUMAN	HS9B_MOUSE HS9B_BRARE	HS9B_CHICK	HS9A_BRARE	HS9A_CHICK	HS9A_HUMAN	HS9A_CRIGR	HS9A_MOUSE	HS9A_PIG	CDB6_HUMAN	CYAA_AERHY
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723	723	725	726	728	731	732	732	732	794	843
67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4
31	31	31	31	31	31	31	31	31	31	31
34	36	3.7	38	39	40	41	42	43	44	45

# ALIGNMENTS

SMART; SM00481; POLITIAC; 1. Transferase: DNA-directed DNA polymerase; DNA replication;

EMBL; AE001649; AAD18805.1; -. EMBL; AE002171; AAF37967.1; -. EMBL; AP002547; BAA98873.1; -.

InterPro; IPR004013; PHP\_C. InterPro; IPR003141; PHP\_N.

CP0081

TIGE;

Pfam; PF02811; PHP\_C; 1 Pfam; PF02231; PHP\_N; 1 1240 AA; 140074 MW; 7D6890EF002A88E4 CRC64;

Complete proteome. SEOUENCE 1240 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20150255; PubMed-10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSTLON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLLII' COMPLEX. POLLII' ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: CYLOPIASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Shii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole grenome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                          .;
0
76.1%; Score 35; DB 1; Length 532; 85.7%; Pred. No. 16; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila,
                                                                                                                                                                                                                                                                                                                                        Chlamydia pneumoniae (Chlamydophila pneumoniae)
                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
bus polymerase 111 alpha subunit (EC 2.7.7.7).
                                                                                                                                                                                                           PRT; 1240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99206606; PubMed-10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20330349; PubMed-10871362;
                    Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                            68 ELDPOTH 74
                                                                        1 ETDPOTH 7
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                                                                                                                                                                                                         DP3A_CHLPN
Q927NB;
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Query Match
                                                                                                                                                                                         A_CHLPN
                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z., "Cloning and functional analysis of CDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoletic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Bone marrow;
MEDLINE-21240216; PubMed-11342114;
MEDLINE-21240216; PubMed-11342114;
"A CDNA from human bone marrow encoding a protein exhibiting homology to the ATPIT/PLM/MATB family of transmembrane proteins.";
to the ATPIT/PLM/MATB family of transmembrane proteins.";
blochim. Blochiys. Acta 1517:307-310(2001).
-- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-- SIMILARITY: BELONGS TO THE FXYD FAMILY.
                                                                                                                                                                                                                           FXY5_HUMAN STANDARD; PRT; 178 AA.
096DB9; Q9P039; Q9HC34;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 5 precursor (HSPC113).
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                            .;
76.1%; score 35; DB 1; Length 1240; 75.0%; Pred. No. 40; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood;
MEDLINE-20499367; PubMed-11042152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (1SOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
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                                          6; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                          525 ETDPDLHQ 532
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                                                                               1 ЕГОРОТНО 8
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                                          Matches
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InterPro; IPR001024; LH2
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                                                                                                                                                       Calcium.
                                                                                                                                                                                                      METAL.
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                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                       MSPSGRLCLTTYGLILPTRGQTLKDTTSSSSADSTIMDIQ
VPTRAPDAVYTELQPTSPTPTWPADETPQPQTQTQQCEGTD
GPLVTDPETHKSTKA -> MQTLSNIPCFCLHGSLLPSTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitzler J.W., Eling T.E.;
"Cloning, sequencing and expression of a 5-lipoxygenase from Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                         FXYD DOMAIN-CONTAINING ION TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                           73.9%; Score 34; DB 1; Length 178; 71.4%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                           ATLS (IN ISOFORM 2).
S -> A (IN DBSNP:1688005).
                                                                                                                                                                                                                                                                                                                          HT -> SH (IN REF. 1).
7429D5A838B75AA1 CRC64;
                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
 EM<sup>B</sup>L; BC009642; AAH09642.1; -.
EMBL; AF177940; AAG09301.1; -.
InterPro; IPR00272; ATPIG1_PLM_MAT8.
Effan; PF02038; ATPIG1_PLM_MAT8.1.
PROSITE: PS01310; FXXD; 1.
Transmembrane; Signal; lonic channel; lon transport;
                                                                                                                                                                                                                                                                                                              /FTId-VAR_012349.
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                           REGULATOR 5
                                                                                                                         POTENTIAL.
                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
                                                                                        Alternative splicing; Polymorphism. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97109716; PubMed=8951996;
                                                                                                                                                                                                                                                                                                                                              19453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U4333; AAA85257.1; -. HSSP; P12530; 1LOX.
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                         178
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164
178
97
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                                                                                                                                                                                                                                                                                                                                              178 AA;
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                                                                                                                                                                         22
146
165
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P51399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- CATALYTIC ACTIVITY: ARACHIDONATE + O(2) - (6E,82,112,14Z)-(5S)-5-HYDROPEROXYCOSA-6,8,11,14-TETRAENOATE (THE PRODUCT IS RAPIDLY CONVERTED TO LEUKOTRIENE A4).
-:- COPACTOR: IRON, ALSO REQUIRES CALCIUM AND ATP FOR ACTIVITY.
-:- PATHWAY: THIS ENZYME CATALYSES THE FIRST TWO STEPS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Balcarek J.M., Theisen T.W., Cook M.N., Varrichio A., Hwang S.-M., Strohsacker M.W., Crooke S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minor W., Steczko J., Bolin J.T., Otwinowski z., Axelrod B.; "Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1."; Blochemistry 32:6320-6323(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Isolation and characterization of a cDNA clone encoding rat 5-
                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                       Oxidoreductase; Dioxygenase; Iron; Leukotriene biosynthesis;
                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 672; Pred. No. 32; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                      1F7234B5C297B30F CRC64;
                                                                                                                                                                                           IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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                                                                                                                                                                           BY SIMILARITY
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J. Biol. Chem. 263;13937-13941(1988).
                                                                                               PROSITE; PS00081; LIPOXYGENASE_2; 1. PROSITE; PS00711; LIPOXYGENASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE+93298753; PubMed-8518276;
       IPR000907; Lipoxygenase.
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TERMINUS DUE TO A FRAMESHIFT.
01-OCT-1989 (Rel. 12, Created)
                                                           PRINTS; PRO0087; LIPOXYGENASE.
SMART; SM00308; LH2; 1.
                                                                                                                                                                                                                                                                    77741 MW;
                                                                                                                                                                                                                                                                                                                            73.98;
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672 AA;
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          295 KTUPCTHQ 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and gene chromosomal assignment of mouse 5-lipoxygenase.";
J. Balol. Chem. 270:17993-17993-17995(1995).
-!- CATALYTIC ACTIVITY: ARACHDONATE + 0(2) * (6E.82,112,142)-(5S)-5-
HYDROPEROXYCOSA-6,8,11,14-TETRAENOATE (THE PRODUCT IS RAPIDLY
CONVERTED TO LEUKOTRENE A4).
-!- CONVERTED TO LEUKOTRENE A4).
-!- COFACTOR: IRON, ALSO REQUIRES CALCIUM AND ATP FOR ACTIVITY.
-!- COFACTOR: IRON, ALSO REQUIRES CALCIUM AND STEPS IN THE
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
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Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae: Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -S., Naumann T.A., Kurre U., Jenkins N.A., Copeland N.G.,
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                                                                                                                                                        PROSITE: PS00081; LIPOXYGENASE_2; 1.
PROSITE: PS00711; LIPOXYGENASE_1; 1.
Oxidoreductase; Dioxygenase; Iron; Leukotriene biosynthesis; Calcium.
                                                                                                                                                                                                                                                IRON (BY SIMILARITY).

** EBBÉSCGÉAPÉBÉCTS CROG4;
                                                                                                                                                                                                                                                                                                                                                                                   73.9%; Score 34; DB 1; Length 672; 75.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSYNTHESIS OF LEUKOTRIENES.
-!- SUBCELLULAR LOCATION: CYLOPIASMIC.
-!- SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6 X 129/SV; TISSUE-Peritoneal cavity; MEDLINE-95355399; PubMcd-7629107;
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                                                           Interpro; IPR001024; LH2.
Interpro; IPR0000907; LH2.
Pfam: PF00305: Iipoxygenase; 1.
Pfam: PF01477; PLAT; I.
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                                                                                                                                                                                                                                                                                                                                   77956 MW;
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              EMBL; J03960; AAA41538.1; -.
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Best Local Similarity
Thes 6; Conserva
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                                PIR; A30882; A30882.
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672 AA;
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                                              P12530;
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MEDLINE-89359178; PubMed-2670911; Choi Y.-L., Nishida T., Kawamukai M., Utsumi R., Sakai H., Komano T.; "Cloning and sequencing of an Escherichia coli gene, nlp, highly homologous to the ner genes of bacteriophages Mu and D108."; J. Bacteriol, 171:5222-5225(1989).
                                                                                                                                                                                                                                                                                                                             Gaps
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SYAAIN-KIZ / MGIGSS,
MEDZINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RILBY M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Maylew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharama T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                             ..
                                                                                        SMART; SM00308; LH2; 1.
PROSTER: PS00081; LLPOXXGENASE_2; 1.
PROSTER: PS0071; LIPOXXGENASE_1; 1.
(xidoreductase; Dioxygenase; Iron; Leukotriene biosynthesis;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 41, Last annotation update)
Sugar fermentation stimulation protein B (Ner-like protein).
SFSB OR NLP OR SFS7 OR B3188 OR 24551 OR ECS4067.
                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 673;
Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                               IRON (BY SIMILARITY).
082910477A3B7085 CRC64;
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IRON (BY SIMILARITY).
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MGD; MGI:87999; Alox5.
InterPro; IPR001024; LH2.
InterPro; IPR000907; Lipoxygenase.
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                                            Pfam; PF00305; lipoxygenase; l.
Pfam; PF01477; PLAT; l.
                                                                           PRINTS; PR00087; LIPOXYGENASE.
                                                                                                                                                                                                                                              77868 MW;
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75.0%;
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673 AA;
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Best Local Similarity
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P18837;
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                                                                                                                                                        Calcium
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STRAIN=0157:H7 / RIMD 0509952;
MREDLINE=21156231; PubMed=11258796;
Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hanashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Tasakawa C., Ogasawara M., Yasunaga T., Rasakawa C., Ogasawara N., Yasunaga T., Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DNA Res. B.11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto Tr., Mori H., Imaseki H.;

"Novel mrna sequences induced by indole-3-acetic acid in sections of elongating hypocotyls of mung bean (Vigna radiata).";

Plant Cell Physiol. 33:13-20(1992).

-!- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME BS AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OT-1993 (Rel. 27, Last sequence update)
01-OR-2002 (Rel. 41, Last annotation update)
0mega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
(Indole-3-acetic acid induced protein ARG1).
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83.3%; Pred. No. 5.8;
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1; Mismatches
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EMBL; AE005547; AAC58322.1; ...
EMBL; AP002564; BAB37490.1; ...
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Best Local Similarity
Matches 5; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JV0027; BVECNP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3916;
                                                                                                                                                                                                                                              REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Heft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamakhavan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makatcva K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last sequence update)
UDP-N-acctylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13) (UDP-N-acctylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase).
-:- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
-:- SUBCELLULAR LOCATION: Endoplasmic reticulum.
-:- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
-!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
-- ND/ OR BE INVOLVED IN METAL ION BINDING.
-- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
glutamate + meso-2,6-diaminoheptanedioate = ADP + phosphate +
UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 33; DB 1; Length 380; 62.5%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1C005117A8DAE16B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HISTIDINE BOX 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTIDINE BOX 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                           IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                                        Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43996 MW;
                                                                                                                                                                                                                                                                            EMBI.: D14410; BAA03306.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus radiodurans.
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231
256
101
137
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ETDPOTHQ 8
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TRANSMEM
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewish-sib.ch).
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MCDOWell K.J., Adams M.H., Baker C.B.;
MCDOWell K.J., Adams M.H., Baker C.B.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE ITEN BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE
TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION
TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO
HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eguus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Serotransferrin precursor (Siderophilin) (Beta-1-metal binding
                                                                                                                                                                                                                                                                                                                                 Pfan: PF01225; Mur_ligase; 1.
Pfam: PF02875; Mur_ligase_C: 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 33; DB 1; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                113 119 ATP (POTENTIAL).
490 AA; 52316 MW; 46C748E9768754CA CRC64;
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i' SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 36; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carpenter M.A., Broad T.E.; "The cDNA sequence of horse transferrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1173:230-232(1993).
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-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                           Interpro; IPR000713; Mur_ligase.
Interpro; IPR004101; Mur_ligase_C.
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                                                                                                                                                                                                                                    EMBL; AE001890; AAF09877.1; -.
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Matches 6; Conservative
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                                                                                                                                                                                                                                                           P11880; 1GG4.
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1A0FA566C0409D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                Iron transport; Glycoprotein; Metal-binding; Repeal; Signal.
SIGNAL 1981 SIMILARITY.
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(BY SIMILARITY).
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(BY SIMILARITY).
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ANION (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                        SEROTRANSFERKIN.
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IRON 2 (BY SIM
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                                                                                                                                                              PROSITE: PS00205; TRANSFERRIN_1; 2. PROSITE; PS00206; TRANSFERRIN_2; 2. PROSITE; PS00207; TRANSFERRIN_3; 2.
                                                                                                                  nterPro; IPR001156; Transferrin.
                                                                                                                            Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
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Similarity 71.4%;
5; Conservative
                                                                       EMBL; M69020; AAA30958.1; -.
                                                                                  AAA63684.1; -.
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                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                             PIR; S33761; S33761.
HSSP; P02787; IA8E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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104 KTEPQTH 110
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094833;
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METAL
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                                                                                                  Nagase T., Ishikawa K., f., Suyama M., Kikuno R., Miyajima N., Tranka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eukaryota; Metazoa; Chordala; Craniala; Vertebrala; Euteleostomi;
Mammalia; Eutheria; Primates: Calarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus/Deinococcus group; Thermus group; Meiothermus
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30-MAY-2000 (Rcl. 39, Last sequence update)
01-MAR-2002 (Rcl. 41, Last annotation update)
Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK).
                                                                                                                                                                          DNA Res. 5:277-286(1998).
-!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
-!- SIMILARITY: CONTAINS 7 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 1065;
Pred. No. 84;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EF-HAND 1 (POTENTIAL),
9 EF-HAND 2 (POTENTIAL),
121325 MW: 1701547C12D4249E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00054; EFh; 2.
SMART; SM00243; GAS2) 1.
SMART; SM0150; SPEC; 5.
PROSITE; PS00018; EF HAND; 2.
ACLID-binding; Cytoskeleton; Calcium-binding; Repeal.
NON_TER
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SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
SPECTRIN 6.
                                                                                      MEDLINE=99087487; PubMed-9872452;
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003108; GAS2...
InterPro; IPR002017; Spectrin.
Pfam; PF00036; efhand; 2.
Pfam; PF02187; GAS2; 1.
                                                                                                                                                                                                                                                                                                                                                           EMBL; AB018271; BAA34448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 1PR002048; EF-hand.
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; PF02187; GAS2; 1.
Pfam; PF00435; spectrin; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
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300
300
520
522
626
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728
1065 AA;
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                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=277;
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CA_BIND
SEQUENCE
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REPEAT
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PROB_MEIRU
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                          Neumivakin L.V.;
Neumivakin L.V.;
Molecular clouding and sequence analysis of the proA gene from
"Molecular clouding and sequence analysis of the proA gene from
thermophilic enhantum Thermus ruber. The thermophilic (WVY-1998) to the EMBL/GenBank/DBJ databases.
-I- FINCTION: Catalyzes the transfer of a phosphate group to glutamate
to form glutamate 5-phosphate which rapidly cyclizes to 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J. F., Flaischmann R.D., Richardson D., Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)
                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                  // (aklichkin S.Y., Zimina M.S., Yurchenko Y.V., Hromov I.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%; Score 32; DB 1; Length 377; 71.4%; Pred. No. 43;
                                                                                                                                                                                                       -i- PATHWAY: Proline biosynthesis pathway; first step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           )., Venter J.C.:
sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase, Kinase, Proline biosynthesis.
SEQUENCE 377 AA, 40591 MW; F637DFE9DDB11155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00902; GLUTAMATE_5_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF082661; AAC72812.1; ALT_INIT.
InterPro; IPR001049; Aakinase.
InterPro; IPR001057; Glut_5_kinase.
InterPro; IPR002478; PUA.
Pfam; PF00696; aakinase; 1.
Pfam; PF01472; PUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; Pubmed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0474; GLUSKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.48
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00359: PUA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EADPRTH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ETDPOTH 7
                                                                                                                                                                                         phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASNS OR BB0101
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051128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                         Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF01336; tRNA-anti; 1.
PRINTS; PR01042; TRNASYNTHASP.
PROSTTE; PS00179; AA_TRNA_LIGASE_II_1; 1.
PROSTTE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sadek C.M., Jalaguier S., Feeney E.P., Aitola M., Damdimopoulos A.E., Pelto-Hulkko M., Gustafsson J.-A.; "Isolation and characterization of AINT: a novel ARNT interacting protein expressed during murine embryonic development."; Mech. Dev. 97:13-26(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-99296831; PubMed-10366448;
Still I.H., Vince P., Cowell J.K.;
The third member of the transforming acidic coiled coil-containing gene family, TACC3, maps in 4pi6, close to translocation breakpoints in multiple myeloma, and is upregulated in various cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CELL GROWTH AND DIFFERENCIATION. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.
CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA(Asn) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAC3_MOUSE STANDAND; PRT; 631 AA. 09JJ11; 09WVK9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Transforming acidic coiled-coil containing protein 3 (ARNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.6%; Score 32; DB 1; Length 466; 71.4%; Pred. No. 54; 0; Indels tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 466 AA; 53600 MW; 2B5900C0E6DBD1F6 CRC64;
              diphosphate + L-asparaginyl-tRNA(ASI).
-! SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                              InterPro; IPR002106; AA_tkNA_ligase_1f.
InterPro; IPR002309; tkNA-synt_2.
InterPro; IPR002312; tkNA-synt_asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-NIH Swiss; TISSUE=Embryo;
MEDLINE-20480355; PubMed=11025203;
                                                                                                                                                                                                                 EMBL; AE001123; AAC66501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 58:165-170(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interacting protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                Q52428; 1B8A.
                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome SEQUENCE 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 ETDPETY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ETDPQTH 7
                                                                                                                                                                                                                                               BB0101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'racc3 or aln'r
                                                                                                                                                                                                                                                  TIGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAC3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
QQ
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**RECEPTOR NUCLEAR TRANSLOCATOR PROTEIN (ARNT) AND ARNT2.

**RECEPTOR NUCLEAR TRANSLOCATOR PROTEIN (ARNT) AND ARNT2.

**ISUBCELLULAR LOCATION: CYCOPIASMIC.

**ISUBCELLULAR LOCATION: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

**ISOBLE SPECIFICITY: BERRYONICALLY EXPRESSED.

**ISOBLE SPECIFICITY: BERRYONICALLY EXPRESSED.

**ISOBLE SPECIFICITY: BERRYONICALLY EXPRESSED.

**ISTENDE SPECIFICITY: BERRYONICALLY EXPRESSED.

**ISTENDE SPECIFICITY: BERRYONICALLY EXPRESSED.

**ISTENDES, THOWN EXPRESSION IS STEEN IN NEUROSPITHELLUM.**

**INTESTINES, THYMUS AND LIVER, AND A MODERATE SIGNAL IS DETECTED IN THE CARTLAGE PRINORIOUM OF DESEDRATION RIBS, TOOTH AND SEED IN THE TISSUE DISTRIBUTION CHANGES SO THAT NO SIGNAL IS DAYS PC, THE TISSUE DISTRIBUTION CHANGES SO THAT NO SIGNAL IS DETECTED IN THE LIVER AND THE SIGNAL HAS DIMINISHED IN OTHER ORGANS.

**IT IS OBSERVED FOR THE FIRST TIME IN THE SALVARY GLAND, THYROLD GLAND AND BROWN FAT AND WAS STRONG IN THE THYMUS, EVE.

**CHANGE IT HIS DESENTANT OF THE STRONG IN THE MAD THE SALER AND MODERATE NOT THE THYMUS, BUT WEAKER AND MODERATE HALLY. IN A BROWN FAT AND WAS STRONG IN THYMUS, BUT WEAKER AND MODERATE HALLY. THE TREATH LINES.

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**CHANGE IT HERE THE TREAT HERE AND THE THYMUS, BUT WEAKER AND MODERATE.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.6%; Score 32; DB 1; Length 631;
83.3%; Pred. No. 75;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED COIL (POTENTIAL).
MISSING (IN ISOFORM 2).
S -> SSHLGNSQ (IN ISOFORM 2).
P -> S (IN REF. 2).
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92D6324D3890E9CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sulfur metabolite repression control protein
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Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 70626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF156934; AAF85763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD25963.1; -.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1341163; Tacc3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               630
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Q00659;
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INTEPPRO; IPRO01810; F-box.

INTEPPRO; IPRO01810; WA40.

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PRINTS; PR00320; GFRCTEINBRPT.

SMART; SM00256; FERX: 1.

SMART; SM00256; FERX: 1.

SMART; SM00256; WA40: 7.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS50082; WD_REPEATS_1: 4.

PROSITE; PS50082; WD_REPEATS_1: 7.

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Search completed: August 7, 2002, 06:47:37 Job time: 209 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# Result Query Description No. Score Match Length DB ID Description 1 46 100.0 249 4 Q960Q0 Q95dGF5 Phomo sapien 2 46 100.0 249 4 Q960R5 Q96dGF5 Phomo sapien 3 9 84.8 4 Q960R5 Q96dF5 Q960F5 Q960F5</

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Harder T.C., Harder M., Vos H., Kulonen K., Kennedy-Stoskopf S., Liess B., Appel M.J., Osterhaus A.D.; "Characterization of phocid herpesvirus-1 and -2 as putative alpha-and gammaherpesviruses of North American and European pinnipeds."; D.Gen. Virol. 77:27-35(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20059514; PubMed-10592042; Kim W.Y., Kim C.Y., Cheong N.E., Choi Y.O., Lee K.O., Lee S.H., Park J.B., Nakano A., Bahk J.D., Cho M.J., Lee S.Y.; "Characterization of two fungal-elicitor induced rice cDNAs encoding functional homologues of the rab-specific GDP-dissociation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                 82.6%; Score 38; DB 12; Length 262; 75.0%; Pred. No. 8.6; Live 1; Mismatches 1; Indels
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PRINTS; PR00891; RABGDIREP.
SEQUENCE 445 AA; 49701 MW; 09EEC9101849F9D3 CRC64;
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SEQUENCE 262 AA; 30101 MW; 83AA01A8BB6D2790 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GDP DISSOCIATION INHIBITOR PROTEIN OSGDI2.
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GDP DISSOCIATION INHIBITOR PROTEIN OSGDII.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.8%; Score 39; DB 10; Length 438; ilarity 75.0%; Pred. No. 9.3; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                     100.0%; Score 46; DB 4; Length 249; 100.0%; Pred. No. 0.21; tive 0; Mismatches 0; Indels
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C-2001 (TrEMBLrel. 19, Last annotation update)
HELICASE-PRIMASE COMPLEX HOMOLOG PROTEIN (FRAGMENT).
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EMBL: AJ401079; CAB94202.1; -.
HSSP; P21856; JGND.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Nishio M., Xu L., Sasaki M., Haga S., Okumoto M., Mori N., Sarkar N.H., Acha-orbea H., Enami J., Imai S., "Complete Nucleotide Sequence of mouse mammary tumor virus from JYG chinese wild mice: absence of bacterial insertion sequences in the cloned viral gag gene." -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS (BY SIMILARITY). SEQUENCE FROM N.A.

MEDLINE-87112944, PubMed-3027377;

Moore R., Dixon M., Smith R.E., Peters G., Dickson C.;

"Complete nucleotide sequence of a milk-transmitted mouse mammary
"Complete nucleotide sequence of a milk-transmitted mouse mammary
translation of gag and pol.";

J. Virol. 61:480-490(1987). 78.3%; Score 36; DB 10; Length 898; ilarity 100.0%; pred. No. 77; Conservative 0; Mismatches 0; Indels POL OR GAG-POL OR GAG PRO POL.

MOUSEs mammary tumor virus.

Viruses: Retroid viruses; Retroviridae; Betaretrovirus.

NCBL\_TaxID=11757; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Arabidopsis thaliana (Mouse-ear cress). 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last segu 01-DEC-2001 (TrEMBLrel. 19, Last anno GAG PRO POL POLYPROTEIN (FRAGMENT). F18B13.31 PROTEIN (FRAGMENT). EMBL; D16249; BAA03767.1; -. HSSP; P03355; 1MML. Breast Cancer 1:89-94(1994). PRELIMINARY; PRELIMINARY; Best Local Similarity Matches 6; Conserv SEQUENCE FROM N.A. SEQUENCE FROM N.A. 46 ETLPOTHU 53 NCB1\_TaxID-3702; PubMed≈11091515; 47 TDPQTH 52 2 TDPQTH 7 Query Match 083393; **09SSB6** 083393 သ σ RESULT RESULT 083393 a δ a DDR REPARENTED TO THE SECOND T ; 0 ; 0 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis. Kim W.Y., Kim C.Y., Cheong N.E., Choi Y.D., Lee K.O., Lee S.H., Park J.B., Nakano A., Bahk J.D., Cho M.J., Lee S.Y.; "Characterization of two fungal-elicitor induced rice cDNAs encoding functional homologues of the rab-specific GDP-dissociation inhibitor."; Gaps Gaps Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza Brandt P., Dose S., Jarke D., Scharfe M., Schon O., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. ; 0 0 80.4%; Score 37; DB 10; Length 445; 75.0%; Pred. No. 24; Query Match 78.3%; Score 36; DB 10; Length 880; Best Local Similarity 87.5%; Pred. No. 75; Matches 7; Conservative 0; Mismatches 1; Indels Bevan M., Brandt P., Dose S., Jarke D., Scharfe M., Schon Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDbJ dalabases. 1; Indels 1; Indels EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL05353; CAA22976.1; -. EMBL; AL161573; CAB81464.1; -. EU Arabidopsis sequencing project; Eubmitted (FEB-1999) to the EMBL/GenBank/DDBJ databases 445 AA; 49559 MW; F3F01C989AEEC277 CRC64; 98423 MW; 5FD1102587BCBBF0 CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 98.4 KDA PROTEIN. 880 AA. 1; Mismatches PRT; MEDLINE-20059514; Pubmed-10592042; InterPro; IPR002005; Rab\_GDI\_REP. Planta 210:143-149(1999). EMBL; AF016897; AAB69871.1; -. HSSP; P21856; ICND. Pfam; PF00996; GDI; 1. PRINTS; PR00891; RABGDIREP. Ouery Match
Best Local Similarity 72.00. PRELIMINARY; F16A16.130 OR AT4G28760. Hypothetical protein SEQUENCE 880 AA; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SECUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=4530; NCBI\_TaxID=3702; 1 ETDPOTHQ 8 1 ETDPOTHQ 8 SEQUENCE **698VU3** 

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Gaps

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0; Indels

0; Mismatches

020 132-2-COPY\_132\_100.18PC

ò g Last sequence update)
Last annotation update)

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PRT; 899 AA

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                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopais.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEQUENCE FROM N.A.
Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
Yamada K., Liu S.X., Pham P.K., Lee J.M., Onodera C.S., Quach H.L.,
Tollomith A.D., Jianq P.X., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Torluni M., Yamamura Y., Yu G., Yu S., Bowser L.,
Kanjin, Meyaren M., Karlin, Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Shinn P., Southwick A., Tracy S.E.,
Shinnozaki K., Davis R.W., Ecker J.R., Theologis A., Tracy S.E.,
Shinnozaki K., Davis R.W., Ecker J.R., Theologis A.,
Full Length cDNA of gene A74928760 (GI:2269731).";
Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                   DNA-binding; Endonuclease; Hydrolase; Nucleotidyltransferase;
Polyprotein; RNA-directed DNA polymerase.
NON TER 1 1 1
SEQUENCE 899 AA; 102359 MW; A78C4F65FF2F0C34 CRC64;
                                                                                                                                                                                           78.3%; Score 36; DB 15; Length 899; 75.0%; Pred. No. 77; 1.1ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 36; DB 10; Length 924; B7.5%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 924 AA; 102903 MW; 10B55CC87876CA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                   1-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                             924 AA
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               Integrase_zn.
InterPro; IPR001037; Integrase_C
                                                        Pfam; PF00552; Integrase: 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
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                         KNaseH.
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7; Conservative
              InterPro, IPR003308; Integr
InterPro, IPR002156; RNaseH
InterPro, IPR001584; Rve.
InterPro, IPR000477; RVTse.
                                                                                                                                                                                                                   Conservative
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01-DEC-2001 (TremBLrel.
                                                                                             PF00665; rve;
PF00078; rvt;
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Best Local Similarity
.... 6; Conserva
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Best Local Similarity
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873 ETDPRPHQ 880
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Q9STH6
ID Q9STH6;
AC Q9STH6;
DT 01-MAY-
DT 01-J0N-
DE PUTATIV
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                                                                                                           Pfam;
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T4C9.190 OR AT4G12350.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCB1_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
Bancroft J., Mewes H.W., Mayer K.F.X., Lencke K., Mannhaupt G.,
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                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO80318; CAB45882.1;
EMBL; ALI61533; CAB78278.1;
                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Pfam: PE00249; myb_DNA-binding: 2.
SMART: SMO03495; SANT; 1.
PROSITE: PS00334; MYB_2: 1.
PROSITE: PS50090; MYB_3; 1.
SEQUENCE 250 AA; 28231 MW; D97D7A56A13D8AB9 CRC64;
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Stracke R., Werber M., Weisshaar B.,
The R2R3-WB gene family in Arabidopsis thaliana.";
Curr. Optin. Plant Biol. 4:447-456(2001).
EMBL: AF175999; AAD53104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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SMART: SM03395; SANT: 2.
PROSITE; PS00037 WYB_L! UNKNOWN_I.
PROSITE; PS00034; WYB_2: 1.
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es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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| 84 EIDPSTHQ 91
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71 TDPYTHQ 77
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022402
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AC P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopteryqii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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0
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                                76.1%; Score 35; DB 10; Length 286;
75.0%; Pred. No. 37;
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                                                     2; Indels
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PROBLE: PRODUCTOR: ZNE GATA, 2.

PROSITE: PS00344; GATA_ZN_FINGER_1: 2.

PROSITE: PS50114; GATA_ZN_FINGER_2: 2.

PROSITE: PS50114; GATA_ZN_FINGER_2: 2.
286 AA; 32402 MW; A266805A0£784A61 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
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InterPro; IPR001164; Znf_GCS.
Pfam; PF00320; GATA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0619; GATAZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.1%;
75.0%;
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Matches 6; Conservative
                                                      6; Conservative
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                                                                                                                                                        PRELIMINARY;
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                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                  120 EIDPSTHQ 127
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 SEQUENCE
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                                                       Matches
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RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman M.H.S., Gomes S.L., Griber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Margina J.P.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marchado J.A.,
RA Machado M.A., Mardeira A.M.B.N., Madeira H.M.F., Marchado J.A.,
RA Machado M.A., Mardeira A.M.B.N., Madeira H.M.F., Marchado J.A.,
RA Machado M.A., Mardeira A.M.B.N., Madeira H.M.F., Marsukuma A.Y.,
RA Machado M.A., Mardeira A.M.B.N., Madeira H.M.F., Marsukuma A.Y.
RA Machado M.A., Marcine E.C., Miyaki C.Y., Monteiro Vitorello C.B.,
RA Machado M.A., Pereira G.A., Pereira H.A. Jr., Pequero J.B.,
RA Delayoro B.R., Pereira R.C., Palmieri D.A., Paris A.,
RA Delayoro B.R., Pereira R.C., Palmieri D.A., Paris A.,
RA Desixoro B.R., Pereira H.A. Jr., Desquero J.B.,
RA G. Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.E.Z., Squeira W.J., Tsuhako M.H.,
RA Asago M.A., Zatz M., Meidanis J., Setubal J.C., Tsuha fastidiosa.";
RA Tago M.A., Zatz M., Meidanis J., Setubal J.S., Vettore A.L.,
RA Tago M.A., Zatz M., Meidanis J., Setubal J.S., Vettore A.L.,
RA Parin A. Peronon, R. Pereira Parin Pathogen Xylella fastidiosa.";
RA Parin A. Peronon, R. Pereira Parin Pathogen Xylella fastidiosa.";
RA Parin A. Peronon, R. Pereira Parin Parin Pathogen Xylella fastidiosa.";
RA Parin A. Peronon, R. Pereira Parin Parin Pathogen Xylella Fastidiosa.";
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Ezaki B., Koyanagi M., Gardner R.C., Matsumoto H.;
"Nucleotide sequence of cDNA for a GDP dissociation inhibitor (GDI)
which is induced by aluminum (Al) ion stress in tobacco cell culture
(Accession No. AFQ12823) (PGR97-133).";
Plant Physiol. 115:314-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 16; Length 425; Pred. No. 56;
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Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA; 46381 MW; 5B1A2C657AFC39E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49702 MW; 5484214FAD3773D3 CRC64;
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U-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, last annotation update)
GDP DISSOCIATION INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 AA
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PRINTS; PR00753; ACCSYNTHASE.
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HSSP; P21856; 1GND.
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62.5%;
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85.7%;
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Best Local Similarity Bo...
6, Conservative
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us-10-020-139-2\_COPY\_137\_100.18PC Med Aug / 00:33:22 2002

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Oy 1 ETDPQTHQ 8 |:||:||: |DD 151 ESDPKTHE 158

Search completed: August 7, 2002, 06:48:10 Job time: 217 sec

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Med Aug / 00:33:10 2002
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us-10-020-139-2\_copy\_139\_150.rag

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 7, 2002, 06:43:38; Search time 29.84 Seconds Run on:

(without alignments)
29.778 Million cell updates/sec

US-10-020-139-2\_COPY\_159\_166

Perfect score:

1 ETDPQTHQ 8

Seguence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1982.DAT:
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1983.DAT:
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1983.DAT:
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1984.DAT:
/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:
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/SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT: // SIDSI/qcgdata/hold-gcnescq/genescqp-embl/AA1997.DAT:\*/SIDSI/qcgdata/hold-gcnescqy/genescqp-embl/AA1998.DAT:\*/SIDSI/qcgdata/hold-genescqy/genescqp-embl/AA1999.DAT:\*/SIDSIJ/qcgdata/hold-genescqy/genescqp-embl/AA2000.DAT:\*/SIDSIJ/qcgdata/hold-genescqy/genescqp-embl/AA2000.DAT:\*/SIDSIJ/qcgdata/hold-genescqy/genescqp-embl/AA2000.DAT:\*/ /SIDSI/gggdata/hold-geneseg/genesegp-embl/AA1991.bMT:\*/SIDSI/gggdata/hold-geneseg/genesegp-embl/AA1992.DAT:\*/SIDSI/gggdata/hold-geneseg/genesegp-embl/AA1993.DAT:\* /SIDS1/gcgdata/hold-yeneseq/geneseqp-embl/AA1994.DAT:\* /SIDS1/qcqdata/hold-geneseq/geneseqp.embl/AA1995.DAF:\*/SIDS1/dcqdata/hold-geneseq/geneseqp.embl/AA1996.DAF:\* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1990.DAT:\* /SIDSI/qcydata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*/SIDSI/qcydata/hold-geneseq/geneseqp-embl/AA1981.DAT:\* A\_Geneseq\_032802:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Peptide #8941 enco	Human brain expres	Human bone marro₩	Peptide #9264 enco	Human parotid secr	Human parotid secr	Human PRO1025 prot	Human secreted pro	Human secreted pro	Human protein segu	Novel human diagno
OI		ABB41435	AAM62308	AAM75111	AAM35227	AAW69221	AAW60682	AAB24069	AAB25765			
DB C		) 22	22	25	22	9 19	3 19	3 21	3 21		22	
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human diagno human diagno	dia	human diagno human diagno	dia	human diagno	dia	dia	ď	human diagno	dia	human diagno	σ	human diagno	dia	n dia	pepti	e #643 encod	109# נ	orain e	one m	#624	± 63	09# ×	_	human diagno								
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4.6	981	284	506	051	22	609	$\simeq$	33	7.8	28	27	26	26	05	795	7	8	33	33	8	26	96	13	60	93	32	19	Š	22	242	92	
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119	16	B T T	20	22	56	56	56	56	27	30	31	31	35	35	35	35	36	36	38	40	44	47	47	47	47	47	47	47	47	51	53	
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## ALIGNMENTS

Human; foetal liver; gene expression; single exon nucleic acid probe. Peptide #8941 encoded by human foetal liver single exon probe. ABB41435 standard; Peptide; 50 AA. 04-FEB-2002 (first entry) ABB41435; RESULT ABB41435

WO200157277-A2.

09-AUG-2001

03-AUG-2000; 2000US-0632366. 21-SEP-2000; 2000US-0234687. 7-SEP-2000; 2000US-0236359. 04-OCT-2000; 2000GB-0024263. 2000US-0180312. 2000US-0207456. 30-JAN-2001; 2001WO-US00669. 2000US-0608408 30-JUN-2000; 04-FEB-2000; 26-MAY-2000; 

Hanzel DK, Chen W, Rank DR; (MOLE-) MOLECULAR DYNAMICS INC Penn SG,

WPI; 2001-483447/52.

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epilepsy and cancers. The present sequence is a protein encoded by one of
               the probes of the invention.
                                       50 AA;
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30-JUN-2000;
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27-SEP-2000;
                                         Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                   liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                           human foetal
                                                                                                                                                                                                                                                          Gaps
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 Human genome-derived single exon nucleic acid probes useful for
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                                                             The invention relates to a single exon nucleic acid probe for
                                     Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                             100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
                                                                           measuring human gene expression in a sample derived from
            analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                        AAM62308 standard; Protein; 50 AA.
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; 2000US-0234687.
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2000US-0608408.
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Matches 8; Conservative
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                Gaps
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                       100.0%; Pred. w...
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2000US-0234687.
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26-MAY-2000; 2000US-0207456.
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Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AA;
                                                                                                                                                                      22. et.dpqthq 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 etdpqthq 29
                                                                                                              1 ETDPQTHQ 8
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Homo sapiens.
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δ
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                        Peptide #9264 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                                   Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW69221 standard; Protein; 249 AA.
                          AAM35227 standard; Protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human parotid secretory protein.
                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B408.
03-AUG-2000; 2000US-052366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                           03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00663.
                                                                   17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Loc 8; Conserve
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AA;
                                                                                                                        genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ETDPQTHQ 8
                                                                                                                                                                 WO200157272-A2.
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                     09-AUG-2001.
                                               AAM35227;
                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69221;
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            AAM35227
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This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hFSP. The protein is pancreas which are associated with high levels of hFSP. The protein is also useful as antifungal, antibacterial antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated in the recombinant protein and this can be used to raise Ab, useful for the diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal tissue; HPSP; Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 46; DB 19; Length 249; 100.0%; Pred. No. 0.91; Live 0; Mismatches 0; Indels (
                                                   /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parotid secretory protein (HPSP).
                                                                                                                                "mature hPSP"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW60682 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                               96US-0034429.
                                                                                                                                                                                                                                                                                                                                         97WO-US23522.
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Best Local Similarity luv....
8; Conservative
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                                                                                                  249
                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duan R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 249 AA;
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                             Peptide
                                                                                                      Protein
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or astrointestinal tissue, e.g. cancer of salivary gland, thyroid, gastrointestinal tract or pancraas, Sjorgen's syndrome, grostate, breast, gastrointestinal tract or pancraas, Sjorgen's syndrome, grostate, breast, data at a strophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists, Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP from natural sources. Expression of HPSP and for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nicleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hypridisation, particularly for disposis and monitoring of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunicatimulant; antianologenic; leukaemia; lymphoid malionancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; profilelial disorder; stromal disorder; blastocoelic disorder; inflammatpry disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a human parotid secretory protein (HPSP). Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps
                                                                                                                                                                                                                                                                                                                                                                                    New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46; DH 19; Length 249; 100.0%; Pred. No. 0.91; ive 0; Mismatches 0; Indels 0;
ulcerative colitis; Crohm's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1025 protein sequence SEQ ID NO:38.
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                                                                                                                                                                                                  96US-0749288.
                                                                                                                                                             97WO-US20651.
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Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                    Bandman O, Goli SK;
                                                                                                                                                                                                                                                                                                                          WPI; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AA;
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                                                                           W09821329-A1.
                                       Homo sapiens.
                                                                                                                                                             07-NOV-1997;
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                                                                                                                   22-MAY-1998
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0290, PR0311, PR0515, PR0105, PR0117, PR0816, PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                          99US-0143048.
99US-0145698.
99WO-US28313.
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99US-0141037.
                                                                                                                                                            2000WO-US00376.
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                                                                                                                                                                                                                                              99WO-US05028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ, Baker ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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Best Local Similarity
--ns 8; Conservat
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W0200053755-A2.
                                                                                                                                                            06-JAN-2000;
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                                                                                                                                                                                                                                              08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1999;
                                                                                  14-SEP-2000.
                                                                                                                                                                                                                                                                                     02-JUN-1999;
                                                                                                                                                                                                                                                                                                                            23-JUN-1999;
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05-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                 04-JAN-2001
                                                                                                                                                     infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human secreted protein amino acid sequence.

The invention relates to sequences AAAA7725-A87774 which encode human secreted proteins that a proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins to fragments to obtain antibodics capable of specifically binding to the secreted proteins. The cDNAs may also be useful in disquostic, foreasic, gene therapy and chromosome mapptung procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoinfmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, obesity, introchondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, chementia, hyperlipidaemia, septic shock and impotence.
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                                                                                         Human, secreted protein; forensic procedure, gene therapy, chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis, hyporhyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
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Ouery Match

Best Local Similarity 100.0%; Pred. No. 0.91;

Matches 8; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Figure 10; 306pp; English.
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                                                 Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0113686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9905-0141032
28-N():-2000 (first entry)
                                                                                                                                                                                                                                                 septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mapping procedures -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 etdpqthg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA87727.
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                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75351;
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiathritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antidacterial; antianaemic; antidacteri; antidacteric; cytostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antidepressant; noctropic; antidactic; cytostatic; neuroprotective; antidepressant; noctropic; antiparkinsonian; infection; antidaphylactic; rheumatoid arthritis; septic shock; pancreatitis; antidanaphylaxis; neuropathology; cardiac anaphylaxis; autoimmunity; cardiac dystunction; neuropathology; cardiac anaphylaxis; autoimmunity; centile disease; haematopoletic disorder; platelet disorder; promise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to 49 Secreted proteins and the CDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 Secreted proteins and the nucleic acids encoding them, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy and for detecting similar sequences in samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46; DB 22; Length 249; 100.0%; Pred. No. 0.91; tive 0; Mismatches 0; Indels C
                                                       Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                     21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                             99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                        6606940-S066
Human secreted protein #10.
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Best Local Similarity
Matches 8; Conserv
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WO200175067-A2.

11-OCT-2001

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AMA25965 The proteins can have activities based on the tissues and AMA25955 to AMA25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antitheumatic; antiarthritids they are expressed in, such as: antiinflammatory; antitheumatic; antiarthritid; immunosuppressive; antiapted; antimutagen; cardiovascular; antianaemic; antiagen; cardiovascular; antianaemic; antiadeptic; cutoratic; cutoratic; cutoratic; outloff antiabthric; osteopathic; dermatological; antiallergic; antiasthmatic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for a protein and polynucleotides are useful for screening for a folsorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fuggal infections, autoimmunity, quentic diseases, heematopoietic disorders, ontenial, and fundamia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancer, multiple sclerosis, depression, anintis, asthma, diabetes, cancer, multiple sclerosis, depression, anintalial and disease, neurodegenerative and anintal anit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 260; 1217pp; English.
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                                                                                                                                                                                                                                                                                                                                                    Liu C, Drmanac Rr;
                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                               22-DEC-2000; 2000WO-US35017.
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Best Local Similarity 100.0.
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                                                                                                                                                                                                                                                                                                                                                                                                    2001-457603/49.
                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEO INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH99686
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                                             WO200153455-A2.
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Homo sapiens.
                                                                                                                                                                                               23-DEC-1999;
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                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                    Tang YT,
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and apping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The configuration of (II). The configuration of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving or restore normal activity of (II) or to the react disease states involving and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polymerical expression or biological activity. The polypeptide and polymerical esquences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and mino acid sequences. ABG00010-ABG00377 represent novel human when man and advances of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (1) and
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ 1D No 55630; 103pp; English.
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                                                                                                                                                                                                                  Tang YT;
                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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Bost Local Similarity 85...
6: Conservative
                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 AA;
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32 tdpdthq 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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11-OCT-2001.
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polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques for sectors normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypurcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; dlagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ 1D No 37199; 103pp; English.
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                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                 31-MAR-2000; 2000US-0540217
                                                                                                                      23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                         WPI; 2001-639362/73.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AA;
                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                            N-PSDB; AAS71027
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                                                                                                                                                                                                                                                                                                                                                                biodiversity
                     11-OCT-2001.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome can gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for informing expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disconders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human of the printed sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 34989; 103pp; English.
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30-MAR-2001; 2001WO-US08631.
                                                                                31-MAK-2000; 2000US-0540217.
                                                                                                                          23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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30-MAK-2001; 2001W0:US08631
 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating alsolopeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating alsolopeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010 ABG3037 represent novel human data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vir./pub/published_pct_sequences.
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                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 54340; 103pp; English.
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                                                                                                                                 Tang YT;
                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
               30-MAR-2001; 2001WO-US08631.
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Best Local Similarity 85.7°
Matches 6; Conservative
                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                               WPI: 2001-639362/73
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                                                                                             (HYSE-) HYSEQ INC
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onlypeptide (II) sequences to isolated pulyidutioning in the into iterates to isolated pulyidutioning the control pulyidution tender to isolated pulyidutioning to polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polyidution contail activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving and the polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and cannon acid sequences. Abgoonto Addia and products dependent on DNA and amino acid sequences. Abgoonto Addia and products dependent on DNA and and amino acid sequences of the invention.
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85.7%; Pred. No. 45;
Live 0; Mismatches 1; Indels
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31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                        (HYSE-) HYSEO INC.
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Sequence 1192, Ap
Sequence 1193, Ap
Sequence 1194, Ap
Sequence 1200, Ap
Sequence 2, Appli
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3, Appli
3, Appli
                                                                 August 7, 2002, 06:43:38 ; Search time 12.96 Seconds (without alignments) 15.078 Million cell updates/sec
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Sequence 52, Appl
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-159-339A-1199
US-08-159-339A-1199
US-08-159-339A-1194
US-08-159-339A-1194
US-08-159-339A-1194
US-08-159-339A-1194
US-08-155-148-3
US-08-16-214-3
US-08-91-148-3
US-08-91-965-76
US-08-91-965-76
US-08-91-965-71
US-08-91-965-71
US-08-803-973-2
US-08-803-973-2
US-08-803-973-2
US-08-11-107-10
US-08-91-999-14
US-08-914-999-18
US-08-914-999-18
US-08-914-999-18
US-08-914-999-18
US-08-914-999-18
US-08-914-999-16
US-08-914-999-16
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein · protein search, using sw model
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Maximum DB seq length: 200000000
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Sequence 12, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1189, Appli
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29, Appl
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TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.6%; Score 32; DB 2; Length 18; 83.3%; Pred. No. 6.2; ive 1; Mismatches 0; Indels
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8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide from HSV-2 glycoprotein G internal
                    US-08-914-999-8
US-08-914-999-8
US-08-914-999-112
US-08-914-999-112
US-08-914-999-12
US-08-914-999-6
US-08-159-139-4-1189
US-08-159-139-1-189
US-09-314-235-29
US-09-314-235-29
US-09-314-235-29
US-09-314-235-29
US-09-314-235-29
US-09-314-913-8
US-09-314-801-33
US-09-347-801-216
US-09-347-801-216
                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/09017205; Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703)816 4100
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 18 amino acids
amino acid
540
724
725
732
760
768
803
1146
                                                                                                                      2221
2221
2292
3316
402
402
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
STREET: 8th Floor, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                             Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02
CLASSIFICATION:
 MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:||
13 TDPKTH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TDPQTH 7
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 STATE:
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Wed Aug / Ub:33:1/ 2002
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us-10-020-139-2\_copy\_139\_100.1al

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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
COMPUTER: 18M Compatible
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.
                                                                                                                              APPLICANT: Marsden, Howard S
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
CORRESPONDENCE ABORESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Match 69.6%; Score 32; DB 2; Length 18;
Local Similarity 83.3%; Pred. No. 6.2;
les 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kubo, Ralph T.
APPLICANT: Kubo, Ralph T.
APPLICANT: Gete, Howard M.
APPLICANT: Gete, Howard M.
APPLICANT: Gete, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twosend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                          ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOLECULE TYPE: peptide from HSV-2 glycoprotein G FRAGMENT TYPE: internal US-09-017-205-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/017, 205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1190, Application US/08159339A Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604-436
                                                               Sequence 52, Application US/09017205
Patent No. 5965357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703)816-4000
(703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                              Virginia
                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22201-4714
                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Arlington
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                                            US-09-017-205-52
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                                                                                                                                                                                                                                                                                                              STATE:
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APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.4%; Score 31; DB 3; L 71.4%; Pred. No. 1.7e+05; tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE TABLES OF Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
                                                                                                                                                                                                                                      REPERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 05-MA-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MA-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber Ellen Lauver
REGISTRATION NUMBER: 32,762
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1192, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          1190:
                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1254
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                     FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-159-339A-1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ETDPQTH 7
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INFORMATION FOR SEQ ID NO: 1194:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM Compatible
                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4 Matches 5; Conservative
                         SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                           single
                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-159-339A-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                         1 ETDPQTH 7
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| ETDPTSH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Gelis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Grew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

IP: 94111-3834
COMPUTER READABLE FORM:
MDDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFRAMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEEX:
                                                                                                                                  018623-005030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-WAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTONEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1193, Application US/08159339A
Patent No. 6037135
                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1192:
                                                                                                                             REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                    TELEFHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-159-339A-1192
                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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| ETDPTSH 7
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67.4%; Score 31; DB 3; Length 9; 71.4%; Pred. No. 1.7e+05; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROJUCTION: 424
PRICATION NUMBER: US U7/926,666
FILING DATE: 07-040-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEDEY: BIEN LAUGH
REFERENCE/DOCKET NUMBER: 32.762
REFERENCE/DOCKET NUMBER: 32.762
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1194, Application US/08159339A ; Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIJ-9404 WO
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/349,915
FILING DATE: 06.DEC-1994
CLASSIFICATION:
                                                                                                     ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: HJ. 94
TELECOMMUNICATION INFORMATION:
TELEFAN: 207-363-0558
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COM
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 TDPOPHK 314
                                                                                                                                                                                              USA
                                                                                                                                                                      STATE: Maine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                         COUNTRY;
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US-08-951-148-3
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                            Gaps
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Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                         Sequence 1200, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION: US APPLICANT: Kubo, Kalph T.
APPLICANT: Grey, Howard M.
APPLICANT: Calis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: USes
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSTESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NIMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION 143.

APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1199
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application PC/TUS9515696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-159-339A-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
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| ETDPASH 7
                                                            1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                 US-08-159-339A-1200
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Gaps
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College
TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
HUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08951148
Patent No. 5811973
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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Gaps
                                                                                                                                                                                                                                                                                                                                                                       67.4%; Score 31; DB 2; Length 425; 71.4%; Pred. No. 2.5e+02; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
ITILE OF INVENTION: CELL DIVISION REGULATORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
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ADDRESSE: ADDRESS: ADDRESS:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/274,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0407 US
TELECOMMUNICATION: 1NPORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/951,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-274-570-3
; Sequence 3, Application US/09274570
; Patent No. 6121019
            INFORMATION FOR SEQ ID NO: 3:
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                                      SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                  ; LIBRARY: LVZNNOT01
; CLONE: 348429
US-09-165-234-3
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                                                                                                                                                               linear
                                                                                                  amino acid
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Best Local Similarity
                                                                                                                                                                                  IMMEDIATE SOURCE:
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LIBRARY: LVZNN
CLONE: 348429
                                                                                                                            STRANDEDNESS:
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                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 31; DB 2; Length 425; 71.4%; Pred. No. 2.5e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09165234
Fatent No. 5928899
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olda
APPLICANT: Bandman, Olda
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/951,148
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                                                                                                                                                                                              REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REERENCE/COCKET NUMBER: PF-
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 650-855-0555
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                               CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 425 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4%
Matches 5; Conservative
                         FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
; LIBRARY: LVZNNOT01
; CLONE: 348429
US-08-951-148-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ETDPQTH 7
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US-09-165-234-3
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APPLICANT: GONZAIGZ C.
APPLICANT: GONZAIGZ C.
APPLICANT: Lange, B.
TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE TITLE OF INVENTION: CENTROSOME FILE REFERENCE: 9882-003
CURRENT APPLICATION NUMBER: US/09/307,143
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COTIXA COTDOLALION
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                         67.4%; Score 31; DB 3; Length 676;
71.4%; Pred. No. 4.1e+02;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%; Score 31; DB 4; Length 724; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBER: US/08/533,669A
22-SEP-1995
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   Patent No. 5834592
   GENERAL INFORMATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     US-09-307-143-6
; Sequence 6, Application US/09307143
; Patent No. 6335157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
            ; TYPE: PRT
; ORGANISM: Bacillus sp.
US-08-947-965-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-307-143-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                      Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                     259 EVDPQNH 265
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                                                                                                                                                       1 ETDPQTH 7
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LENGTH: 724
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                                                                                          Query Match
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      Gaps
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      0;
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                                                                                                                                    67.4%; Score 31; DB 3; Length 675; 71.4%; Pred. No. 4e+02; tive 0: Mismatches 2; Indels
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APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkstra, Bauke
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Osten, Claus von der
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
FILE REFERNCE: 4285.204-05
CURRENT APPLICATION NUMBER: US/08/947,965A
CURRENT FILING DATE: 1995-04-21
EARLIER FILING DATE: 1995-04-21
EARLIER FILING DATE: 1995-01-16
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1996-04-22
NUMBER OF SEQ ID NOS: 78
SOFTHARE: FastsEQ for Windows Version 3.0
     1; Indels
 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/08947965A
Patent No. 6004790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bacillus obbensis
US-08-947-965-76
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Best Local Similarity 71.4%
For the Similarity 71.4%
5; Conservative
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                             1 ETDPQTH 7
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US-08-947-965-76
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LENGTH: 676
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Matches
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| TELECOMMUNICATION INFORMATION: | TELECOMMUNICATION INFORMATION: | TELEPHONE: (206) 622-4900 | TELEFAX: (206) 682-6031 | TAPE: amino acida | TAPE: amino ac
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August 6, 2002, 17:05:16; Search time 66.51 Seconds (without alignments) 13.003 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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51
1 DNPQHKTQL 9
                                                                           OM protein - protein search, using sw model
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                                                                                                               Run on:
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283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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		ID	VHIV34	VHIVXL	VH1V68	VH1V61	VHIVA7	VHIVAK	VHIVNS	VHIV8H	VHIVN7	VHIVXŞ	VHIVX3	VHIVX4	VHIVX5	VHIVX6	6NAIHA	VHIVN6	VHIVN3	VHIVN2	VHIVNI	VHIVC1	VHIVM1	A60028	VHIVA3	VHIVA6	VHIVX1	VHIVN8	VHIVN4	B36754	A42757	
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nucleoprotein - in hypothetical 12.1 hypothetical prote hypothetical prote UDP-Nacetylmuramy bypothetical prote conserved hypothet membrane protein [hypothetical 66.6 hypothetical 66.6 hypothetical prote probable membrane conserved hypothet prote probable membrane probable membrane probable beta-phos probable beta-phos hypothetical prote	/34) 82 #text_c} nucleoprote Devos, R.; 6-429,'N',4	Store 37; DB 1: Length 498; Pred. No. 19; Thismatches 1: Indels 0; Gaps 0; Strain X/Leningrad/54/1 [HIN1]) Sion 31-Mar-1993 #text_change 16-Jul-1999 Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; guencing of a full-length DNA copy of NP gene of t 5307106 Signature 2324691; PIDN:AAA43459.1; PID:g324692 codon GUG for residue 67 as Ala
S34418 H65096 E91124 D9750969 D97162 AC2372 AC2372 AC2372 AC2372 AC65202 AC6936 C90343 T45875 T45875 S73706	ALIGNMENT ision 17-Dec 777 ne encoding t 82041445 ,354-424,''' HON1 cleoprotein	virus (strain X/Len an) virus
попопопопопопоп	virus e_rev A040 e gen MUID:: HU: 1982	virus
498 104 104 482 271 271 577 577 577 577 577 577 577 577 577 5	influenza A virus enza A virus 982 # sequence 327; A94590; a1428, 1981 ucture of the err. A94327; Min Jou, W. Atlas, June err. A94590 apenomic RNA Atlas, June arr. A94890 apenomic RNA Atlas, June Atlas, June arr. A94890 apenomic RNA arr. Applement a substringent arr. Applement a substringent arr. Applement a substringent arr. Arr. Arr. Arr. Arr. Arr. Arr. Arr.	12.5% Conservative Conservative FOL 9 FOL 328
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ш ш ш ш ш ш ш ш ш 4 4 4 4 4 4 О ш И ш 4 ш 0 Г 0 В 0 О П И ш 4 В	RESULT VHIV34 nucleoprotein - influenza A virus (strain A/PR/8 C;Species: influenza A virus (strain A/PR/8 C;Species: influenza A virus (strain A/PR/8 C;Species: influenza A virus (strain A/PR/8 C;Date: 18-Aug-1982 #sequence_revision 17-Dec-19 C;Accession: Ag127; Ag1590; A04077 R;Winfer, G.; Fields, S. Virology 114, 423-428, 1981 A;Title: The structure of the gene encoding the A;Reference number: Ag1327 A;Wolecule type: genomic RNA A;Residues: 1-498 <anin> R;Van Rompuy, L.; Min Jou, W.; Huylebroeck, D.; Submitted to the Atlas, June 1982 A;Residues: 1-496 <anin> A;Residues: 1-246, W., 248-332, L', 354-424, 'I', 42 A;Residues: 1-246, 'N', 248-332, L', 354-424, 'I', 42 A;Reperimental source: substrain HON] C;Genetics: A;Map position: segment 5 C;Superfamily: influenza virus nucleoprotein</anin></anin>	Ouery Match Best Local S Matches Oy 1 DNPO D 320 ENPA NESULT 2 VHUXL C) Species inf A) Note: host He C) Date: 31-Mar C) C) Cote: South A) Reference nu A) Reference nu A) Residues: 1-C A) Cross-reference A) Note: the aut C) Genetics: C) A) Genetics: C) A) Genetics: C) A) Genetics: C) C) Genetics: C) C) Cote: C)
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nucleoprotein - influenza A virus (strain A/Udorn/307/72)
C:Species: influenza A virus
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Date: 31-Mar-1988 #sequence 305672
R:Buckler-White, A.J.; Murphy, B.R.
Virology 155, 345-355, 1986
A:Title: Nucleoprotide sequence analysis of the nucleoprotein gene of an avian and a hum A:Reference number: A94345; MUID:87071656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-498 ~CBUC>
A; Cross-references: GB:M14922; NID:g325098; PIDN:AAA43686.1; PID:g325099
A; Cross-references: strain A/Udorn/307/72
A; Experimental source: strain A/Udorn/307/72
B; Altureller, A.; Fitch, W.M. Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
A; Title: Biological and genetic evolution of the nucleoprotein gene of human influenz
A; Reference number: A36754; MUID:89361370
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C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein: phosphoprotein
F:176.345/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                              .;
                                                               Score 37; DB 1; Length 498;
Pred. No. 19;
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C;Species: influenza A virus
                                                                                                                                                              1; Indels
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66.7%; Pred. No. 19;
live 2; Mismatches
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                                                                                                                                                              2; Mismatches
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                                                          72.5%;
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                                                                                                                                                         Conservative
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          Query Match
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A; Residues: 1-498 <ALT>
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Matches 6; Conserv
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C;Species: influenza A virus
C;Date: 3.Dec-1990 #sequence_revision 31-Dec-1990 #text_change 08-Apr-1994
C;Accession: D31831
R;Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.
A;Viclogy 167, 554-567, 1988
A;Title: Identification of sequence changes in the cold-adapted, live attenuated influen
A;Reference number: A31831: MUID:89073759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The sequence of the nucleoprotein gene of human influenza A virus, strain A/NT/
A;Reference number: A04078; MUID:82150233
A;Accession: A04078
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J. Gen. Virol. 70, 2111-2119, 1989
A;Title: Biological and genetic evolution of the nucleoprotein gene of human influenza
A;Reference number: A36754; MUID:89361370
A;Stetus: preliminary
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C;Species: Influenza A virus
C;Cate: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A04078; Fi20678
C;Accession: A04078
C;Acces
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A:Experimental source: strain A/NT/60/68
A:Map position: segment 5
C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein: phosphoprotein
F:176,345/Binding site: phosphate (Ser) (covalent) #status predicted
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19;
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Pred. No. 19;
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C;Superfamily: influenza virus nucleoprotein
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C;Superfamily: influenza virus nucleoprotein
C;Keywor&s: nucleoprotein
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Pred. No.
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66.7%;
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Best Local Similarity
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A; Residues: 1-498 <ALT>
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320 ENPAHKSQL 328
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N.Alternate names: NP protein
C.Species: Influenza A virus
C.Date: 30.58p-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C.Accession: G31470
R.Gammellin, M.; Mandler, J.; Scholtissek, C.
R.Gammellin, M.; Mandler, J.; Scholtissek, C.
A.Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A.Reference number: A31470; MUID:89243210
A.Molecule type: genomic RNA
A.Rocession: G31470
A.Molecule type: genomic RNA
A.Rocession: G31470
A.Molecule type: GB:M22571; GB:J04339; NID:9325058; PIDN:AAA43668.1; PID:9325059
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C.Species: influenza A virus
A.Species: infl
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N;Alternate names: NP protein
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2; Mismatches
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C;Superfamily: influenza virus nucleoprutein
C;Keywords: nucleoprotein
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C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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320 ENPAHKSQL:328
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C;Species: influenza A virus
C;Species: 11-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: 805502
R;Reinhardt, U.; Mandler, J.; Scholtissek, C.
Nucleic Acids Res. 17, 6721, 1989
A;Title: Sequence of the nucleoprotein (NP) gene of the influenza A virus reassortant 81
A;Reference number: 805502
A;Accession: 805502
A;Accession: 805502
A;Residues: 1-498 <REI>
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A. Residues: 1-498 cGAM>
B. A. M. W. Scholussek, C.
J. Gen. Virol. 70, 2111-2119, 1989
A. Title: Blological and genetic evolution of the nucleoprotein gene of human influenza A. Reference number: A36754; MUID:89361370
A. Reference number: A36755
A. Schaus: Preliminary
A. Molecule type: genomic RNA
A. Reference number: A168 cALT>
B. Superfamily: influenza virus nucleoprotein
C. Keywords: nucleoprotein
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C; Species: influence. A virus
C; Date: 30 Sep-1990 #sequence_revision 30 Sep-1990 #text_change 16-Jul-1999
C; Accession: E31470; H36755
R; Gammelin, M.; Mandler, J.; Scholtissek, C.
A; Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A; Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A; Accession: E31470
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C:Genetics:
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                                     72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19;
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66.7%; Pred. No. 19;
tive 2; Mismatches
                                                                       Pred. No. 19;
2; Mismatches
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C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
Query Match
Best Local Similarity 66.7.
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A:Map position: segment 5
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                                                                                                                             A;Title: Biological and genetic evolution of the nucleoprotein gene of human influenza A
A;Reference number: A36754; MUID:89361370
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A;Note: host Homo sapiens (man)
C;Accession: H36754; Pod411; Pod423
B;Altimeller, A.; Fitch, W.M.; Scholtissek, C.
A;Title: Bological and genetic evolution of the nucleoprotein gene of human influenza.
A;Ritle: Balogical and genetic evolution of the nucleoprotein gene of human influenza.
A;Reference number: A36754; MUID:89361370
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J. Gen. Virol. 70, 2111-2219, 1989
A;Title: Biological and genetic evolution of the nucleoprotein gene of human influenza
A;Referance number: A36754; MUID:89361370
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                   A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
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Pred. No. 19;
2; Mismatches 1; Indels
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N;Alternate names: NP protein
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66.7%; Pred. No. 19;
tive 2; Mismatches
                                                         C,Accession: D36754
R;Altmueller, A.: Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
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C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
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C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
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66.7%;
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Best Local Similarity 65.00
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C;Species: influenza A virus
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C;Species: influenza A virus
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A; Residues: 1-498 <ALT>
C; Genetics:
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A; Residues: 1-498 <ALT>
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320 ENPAHKSQL 328
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A; Residues: 1-498 <ALT>
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A;Cross-references: GB:D00602; NID:g221289; PIDN:BAA00478.1; PID:g221290
A;Experimental source: strain A/Texas [H3N2]
A;Experimental source: strain A/Texas [H3N2]
J. Gen. Virol. 73, 1329-1337, 1992
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A;Accession: PQ0408; MUD:92300326
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J. Gen. Virol. 70, 2111-2119, 1989
A;Tille: Biological and genetic evolution of the nucleoprotein gene of human influenz
A;Reference number: A36754; MUID:89361370
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C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: A36755
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Cispecies: influenza A virus
Cispecies: influenza A virus
Cispecies: 30-sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
CiAccession: I3470
Ridamellin, M: Mandler, J.; Scholtissek, C.
Wirology 170, 71-80, 1989
A:Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A:Reference number: A31470; MUID:89243210
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A;Residues: 1-498 <ALT>
A;Cross-references: GB:D00600; NID:g221285; PIDN:BAA00476.1; PID:g221286
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Pred. No. 19;
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A;Residues: 23-55 <L1A2>
A:Experimental source: strain A/Guizhou/54/89 [H3N2]
C;Genetics:
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A;Residues: 23-55 <LIA1>
A:Experimental source: strain A/Hebei/24/89 (H1N2)
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C:Superfamily: influenza virus nucleoprotein
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Matches 6; Conservative
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C;Species: influenza A virus
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A; Accession: 131470
A;Molecule type: genomic RNA
A;Rosidues: 1-498 cGAM>
A;Cross-references: GB:M22578; GB:J04339; NID:g325071; PIDN:AAA43676.1; PID:g325072
C;Genetics:
A;Gene: NP
A;Gene: NP
A;Gene: NP
C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
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Db 320 ENPAHKSQL 328
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Search completed: August 6, 2002, 17:05:17 Job time: 919 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein . protein search, using sw model

August 6, 2002, 17:07:36 ; Search time 32.88 Seconds (without alignments) 10.598 Million cell updates/sec

US-10-020-139-2\_COPY\_237\_245 51 1 DNPQHKTQL 9 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

P26068 influenza a	P15673 influenza a	P16979 influenza a	٠	P16982 influenza a	P16980 influenza a	P15674 influenza a	P16314 influenza a	091743 influenza a	P31609 influenza a	P15675 influenza a	P06826 influenza a
VNUC_1AHJ1	VNUC_IAHLO	VNUC_IAHMI	VNUC_IAHO1	VNUC_IAHO2	VNUC_IAHPR	VNUC_IAHTE	VNUC_IAKIE	VNUC_IAKIT	VNUC_IALEN	VNUC_IAMAA	VNUC_IAMAN
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72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5
37	37	3.7	37	37	37	37	37	37	37	37	37
34	35	36	3.7	38	39	40	4.1	42	43	44	45

#### ALIGNMENTS

KESULT ] VNUC_IAANA	ID VNUC JAANA STANDARD: PKT; 498 AA. AC P18277;	01-NOV-1990 (Rel. 16, Creat	01-JUN-1994	in.		-			OX NCHI_TaxID=11323;			MEDLINE=91288235; PubMed=2062661;	Mandler J., Kunerl M.S., Ludwig S.,	"Sequence of the nucleoprotein (NP)					This SWISS-PROT entry is copyright. It is produced through a collaboration		the European Bioinformatics institute. There are no restrictions on	200	entities requires a license agreement (See	_					KW Nucleoprotein.	SQ SEQUENCE 498 AA; 56348 MW; 809E162F61077244 CRC64;	72.5%; Score 37;	Dest Local Similarity 66.7%; Pred. No. 8.3; Matches 6; Conservative 2; Mismatches 1: Indels 0: Gaps 0;	
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VNUC\_IAANN STANDARD; PRT; 498 AA. P21433; P80881; 01-MY-1991 (Rel. 18, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Nucleoprotein. RESULT 2 VNUC\_IAANN ID VNUC\_IA AC P21433; DT 01-MAY-DT 01-NOV-DT 01-NOV-DE NUCleop

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                                                                                                                                                              MEDLINE=89073759; PubMed-2974219; COX N.J., Kitame F., Kendal A.P., Maassab H.F., Naeve C.; COX N.J., Kitame F., Kendal A.P., Maassab H.F., Naeve C.; Identification of sequence changes in the cold-adapted, live attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2)."; Virology 167:554-567(1988).
i. FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT 23 23 N -> T (IN COLD-ADAPTED ISOLATE). VARIANT 34 34 G -> D (IN COLD-ADAPTED ISOLATE). SEQUENCE 498 Aa; 55963 MW; E51D08494E9FA075 CRC64;
                                   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                  Influenza A virus (strain A/Ann Arbor/6/60)
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InterPro; IPR002141; Flu_NP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00506; Flu_NP; 1.
                                                                                                        NCBI_TaxID=135322;
                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleoprotein.
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EMBL, L07373; AAA51490.1; EMBL, L07373; AAA51489.1; EMBL, L07370; AAA5151.1; EMBL, L07370; AAA5148.1; EMBL; L07353; AAA51485.1; EMBL, L07353; AAA51484.1;

InterPro; IPRO02141; Flu\_NP. Pfam; PF00506; Flu\_NP; 1.

EMBL; 1,07374; AAA51486.1; -.

0 72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3; ative 2; Mismatches 1; Indels Best Local Similarity 66.73 Matches 6; Conservative Query Match

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320 ENPAHKSOL 328 1 DNPQHKTQL 9 pp

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                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE-9323329; PubMed-8474171;
Shu L.L., Bean W.J., Webster R.G.;
Analysis of the evolution and variation of the human influenza A
virus nucleoprotein gene from 1933 to 1990.";
J. Virol. 67:2723-2729(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -: - FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                           influenza A virus (strain A/Beijing/337/89),
Influenza A virus (strain A/Beijing/352/89),
Influenza A virus (strain A/Beijing/353/89),
Influenza A virus (strain A/Guangdong/38/89),
Influenza A virus (strain A/Memphis/14/85),
Influenza A virus (strain A/Memphis/8/88),
Influenza A virus (strain A/Memphis/8/88),
Influenza A virus (strain A/Memphis/8/88),
              VINC_1AB37 STANDARD; PRT; 498 AA. 007539; 008029; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         Influenza A virus.
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                                                                                                             Nucleoprotein.
VNUC_IAB37
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1 DNPQHKTQL 9

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MEDLINE-9323329; Pubmed-8474171;
Shu L.L., Bean w.J., Webster R.G.;
Analysis of the evolution and variation of the human influenza virus nucleoprotein gene from 1933 to 1990.";
J. Virol. 67:2723-2729(1993).
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Post Local Similarity 66.7%; Pred. No. 8.3;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Beijing/39/75).
Viruses: ssRNA negative-strand viruses: Orthomyxoviridae:
Influenza virus A and B group; Influenza A viruses:
Influenza A virus.
                                                                                                                                                                                                                                                                                                   72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
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                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498 AA; 56180 MW; C4C61E024F1AA2C1 CRC64;
                                                                                                                                                                                                                                                         498 AA; 56224 MW; 28F46CA5BBD1DAC4 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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Pfam; PF00506; Flu_NP; l.
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Best Local Similarity 60...
6, Conservative
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SEQUENCE 49
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Nucleoprotein.
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SEQUENCE 498
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P18070;
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                               Altmeller A., Fitch W.M., Scholtissek C.; "Biological and genetic evolution of the nucleoprotein gene of human
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Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.;
"Evolution of the nucleoprotein gene of influenza A virus.";
J. Virol. 64:1487-1497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.5%; Score 37; DB 1; Length 498; Best Local Similarity 66.7%; Pred. No. 8.3; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                              Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                  J. Gen. Virol. 70:2111-2119(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 AA; 55988 MW; 4B09757425A7F8DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (strain A/Budgerigar/Hokkaido/1/77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-APR-1990 (Rel. 14, Created)
Ol-APR-1990 (Rel. 14, Last sequence update)
Ol-MAY-1992 (Rel. 22, Last annotation update)
                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                    Influenza A virus (strain A/Brazil/11/78).
                                                                                                                                                                                                                                      MEDLINE=89361370; PubMed=2769232;
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InterPro; IPR002141; Flu_NP.
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  320 ENPAHKSQL 328
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P15660;
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P18069;
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                                                            VNUC_IABRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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-i- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                     498 AA; 56291 MW; 43990247E22774EB CRC64;
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66.7%; Pred. No. 8.3;
Live 2; Mismatches
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01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
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InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
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Pfam; PF00506; Flu_NP; 1.
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Best Local Similarity
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                                                                                                                                                                                                                      Reinhardt U., Scholtissek C.; "Comparison of the nucleoprotein genes of a chicken and a mink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90204657; Pubmed-2319644; MeDLINE-90204657; Pubmed-2319644; Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.; Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.; Evolution of the nucleoprotein gene of influenza A virus."; J. Virol. 64:1487-1497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Chicken/Pennsylvania/1/83).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenca virus A and B group; Influenca A viruses;
Influenca A virus.
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-!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 AA; 56235 MW; ECEEADC066E72FE9 CKC64;
                                                                                                                    Influenza A virus (strain A/Chicken/Germany/n/49).
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01-APR-1990 (Rel. 14, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
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                          PRT;
                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89104698; Pubmed-3214270;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M24453; AAA43470.1; -.
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InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
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Best Local Similarity 66...
6; Conservative
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320 ENPAHKSQL 328
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NCBI_TaxID=11341;
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                                                                                             Nucleoprotein.
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P15661;
                          VNUC_IACKG
P16984;
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  RESULT 8
VNUC_IACKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDIINE-91251223; Pubmed-2041090; Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y., Gorman O.T., Each W.J., Kawaoka I., Donatelli I., Guo Y., Webster R.G.; "Evolution of influenza A virus nucleoprotein genes: implications for the origins of HINI human and classical swine viruses.";
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                                                                                                                                                                                                                                                                                                                    Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Duck/Australia/749/80).
Viruses: ssRNA negative-strand viruses: Orthomyxoviridae;
Influenza virus A and B group: Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                            498 AA; 56274 MW; HFD13C3A68DB4BAB CRC64;
                                                                                                                                                                                                                                                                                                                    Score 37; DB 1;
Pred. No. 8.3;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
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66.7%;
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                                                                                                                                                              InterPro; IPR002141; Flu_NP. Pfam; PF00506; Flu_NP; 1.
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Best Local Similarity 66./
The Gooservative
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Best Local Similarity bb...
6; Conservative
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VNUC_IADBE
ID VNUC_IADBE
AC P26064;
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P26065;
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Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.;
"Evolution of the nucleoprotein gene of influenza A virus.";
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tive 2; Mismatches 1; Indels
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridue;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                           Influenza A virus (strain A/Duck/Beijing/1/78).
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01-APR-1990 (Rel. 14, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
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                                                          Nucleoprotein.
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P15662;
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- VIVOL. 65:3704-3714(1991).

- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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66.7%; Pred. No. 8.3;
Live 2; Mismatches 1; Indels
                                                                                                                                   72.5%; Score 37; DB 1; Length 498.
66.7%; Pred. No. 8.3;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Duck/England/1/56).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91251223; PubMed-2041090;
Gorman O.T., Bean W.J., Kawacka Y., Donatelli I., Guo Y.,
Webster R.G.;
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                                                                                   498 AA; 56244 MW; D393CD14859491ED CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
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                              InterPro; IPR002141; Flu_NP. Pfam; PF00506; Flu_NP; 1.
               EMBL; M30762; AAA43483.1; -
                                                                                                                      Query Match
Best Local Similarity 60.7.
Loca 6, Conservative
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Matches 6; Conservative
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P26062;
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P26063;
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                                                                                                                                                                                                       "Evolution of influenza A virus nucleoprotein genes: implications for the origins of HNI human and classical swine viruses.";
J. Virol. 65:3704-3714(191).
J. Virol. 65:3704-3714(191).
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"Two subtypes of nucleoproteins (NP) of influenza A viruses.";
Virology 170:71-80(1989).
-i- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
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            Influenza A virus (strain A/Duck/England/1/62).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Influenza virus A and B group; Influenza A viruses;
                                                                                                                                             MEDLINE-91251223; Pubmed-2041090;
Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 AA; 56328 MW; 5F0EA230D13C31C0 CRC64;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-MAY-1992 (Rel. 22, Last annolation update)
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InterPro; IPR002141; Flu_NP.
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Best Local Similarity 66.73
Matches 6; Conservative
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                                                                        Influenza A virus.
NCBI_TaxID=11355;
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P16978;
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PRELIMINARY;
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1 DNPQHKTQL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tracey A.;
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Q9BQQ0;
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13.983 Million cell updates/sec
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096dr5 homo sapien
007163 mycoplasma
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                                                                                           August 6, 2002, 17:09:32; Search time 111.35 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
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Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Q96DR5
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sp_unclassified:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AL121901; CAC03546.1; -- SEQUENCE 249 AA; 27011 MW; E64E0794A1B4DB7D CRC64;
                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49010.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30).
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01-DEC-2001 (TrEMBLrel. 19, Last anno
PAROTID.SECRETORY PROTEIN.
HOMO sapiens (Human).
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                   Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPT proteins is expressed in the human parolid gland."
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF432917; AAL28113.1;
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=155225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 4; Length 249; 100.0%; Pred. No. 0.03;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TTEMBLEL. 04, Created)
01-JUL-1997 (TTEMBLEL. 04, Last sequence update)
01-JUL-1997 (TEMBLEL. 04, Last annotation update)
PCL42-56 IMMUNODOMINANT MEMBRANE PROTEIN (FRAGMENT).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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STRAIN-A/HONG KONG/507/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
les 9; Conservative
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Matches 7; Conservative
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                                                                                                                               SEQUENCE FROM N.A.
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                                                          NCBI_TaxID=9606;
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                                                                                                                                                              TISSUE-PAROTID;
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Influenza A virus (A/Netherlands/001/94 (H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=132729;
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Subbarao K.;
"Avian influenza A HSN1 and H9N2 viruses bearing a specific constellation of nouglycoprotein genes caused illness in humans.";
Submitted (APR-2000) to the EMBL/GenBank/NDBJ databases.
EMBL; AF255763; AAK49289.1;
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Wecten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaen G.F.;
"Antigenic drift in the Influenza A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225709; AARPS33.1, ...
DIGEPRO: IPR002141; Flu_NP.
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121 AA; 13295 MW; 2DEE1A250286E685 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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NUCLEOPROTEIN (FRAGMENT)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
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MEDLINE=20347342; PubMed=10888619;
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58 ENPAHKSQL 66
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132731;
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Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132730;
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Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A., Osterhaus A.D., Rimmelzwaan G.F.; Antigenie drift in the influenza A virus (H3N2) nucleoprotein and escape from recognition by cytotoxic T lymphocytes."; J. Virol. 74:6800-6807(2000).

EMBL; AF225710; AAF87331.1; -
PinterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
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SEQUENCE FROM N.A.

WEDLINE-20347342; PubMed=10886619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.,
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL, AF225711; AAF87332.1;
InterPro; IPR002141; Flu_NP.
Pfam. PF00506; Flu_NP; 1.
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152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
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Best Local Similarity 66.73
Matches 6; Conservative
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Matches 6; Conservative
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Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132732;
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        SEQUENCE FROM N.A.
MEDLINE=20347342; PubMed=10888619;
MEDLINE=20347342; PubMed=10888619;
Octen J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.,
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
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MEDLINE-20347342; Pubmed-1088619;
MEDLINE-20347342: Pubmed-1088619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
secape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225713; AAF87334.1;
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Live 2; Mismatches 1; Indels
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SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
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                                                                                                       J. Virol. 74:6800-080/(2007).
BMBL: AF225/12: ARE8733.1; -.
InterPro; IPR002141; Flu_NP.
Pfam: PP00506; Flu_NP: 1.
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Pfam; PF00506; Flu_NP; 1.
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Best Local Similarity 66.79
Matches 6; Conservative
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Q911F8
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Influenza A virus (A/Netherlands/021/94 (H3N2)).
Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza a virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TAXID-132736;
                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID-132735;
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"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and escape from recognition by cytotoxic T lymphocytes.";

J. Virol. 74:6800-6807(2000).

EMBL, AF225717; AAF8738.1;

PinterPro: IPR002141; Flu_NP.

Pfam: PF00506; Flu_NP: 1.

NON_TER
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J. Virol. 74:6800-6807(2000).

J. InterPro: IPR002141; Flu.NP.

Priam; PF00506; Flu.NP: 1.
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NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                 Influenza A virus (A/Netherlands/020/94 (H3N2)).
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2; Mismatches
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                                                                                                                                            MEDLINE-20347342; PubMed-10888619;
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Best Local Similarity bo...
6, Conservative
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NUCLEOPROTEIN (FRAGMENT).
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81 ENPAHKSQL 89
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Q9IIF4;
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Influenza virus A and B group; Influenza A viruses; Influenza A virus.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigonic drift in the influenza A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225715; AAF87335.1;
TherePro: JPR002141; Flu_NP.
Pfam: PF00566; Flu_NP: 1.
                                                                                MEDLINE-20147342: Pubmed-10888619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Kimmelzwaan G.F.;
Antiegenic drift in the influence A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800.6807(2000).
ENBL, AF225714; AAF8735.1;
ENBL, AF225714; AAF8735.1;
Pfam: PF00506; Flu_NP:
NON_TER
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                                                                                                                                                                                                                                                                                                                                                72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11; tive 2; Mismatches 1; Indels
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SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                   NCBI_TaxID=132733;
                                                                          SEQUENCE FROM N.A.
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81 ENPAHKSQL 89
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132738;
                                                                                     Influenza A virus (A/Netherlands/022/94 (H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxxviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132737;
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WEDLINE=20347342. Pubmed=10888619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225718; AA+87339.1;
InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP: 1.
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SEQUENCE FROM N.A.

WEDLIKE=20347342; Pubmed=10888619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL, AF225719; AAF87340.1;
InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP:
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NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
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152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Matches 6, Conservative
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Q9IIF3
ID Q9IIF3
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1 DNPQHKTQL 9

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Search completed: August 6, 2002, 17:09:32
Job time: 934 sec
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August 6, 2002, 16:52:54; Search time 138.55 Seconds (Without alignments) 7.215 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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51
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human parotid secr	Human PROIDES prot	Human secreted pro	Equine influence v	SIV strain HiN1 nu	SIV strain H3N2 nu Swinepox virus Hin
SUMMARIES	AAW69221 AAW60682	AAB24069 AAB25765	AAB75351 AAM25745	AAE09054 AAE09053	AAW68409	AAW68407 AAW55986
DB	19	21	22	22	19	19
% Query Match Length DB	2 4 4 4 9	249	249	217	498	4 9 8 4 9 9
% Query Match	100.0	100.0	100.0	72.5	72.5	72.5
Score	51	51	51	37	37	37
Result No.	2	ю <del>4</del>	S 90	٠ 8	σ,	110

PE binding/translo PE binding and tran E. coli proliferat Amino acid sequenc Drosophia melanog Escherichia melanog Escherichia melanog Escherichia melanog Escherichia elipiania Equine influenza v	Drosophila melanog Sequence of the P4 Novel numan diagno Propionibacterium Propionibacterium Arabidopsis thalia Arabidopsis thalia Metal regulated tr Neisseria gonorrho Neisseria meningit A. Gossphila melanog Drosophila melanog Drosophila melanog Protein #5035 enco S. pneumoniae glut Streptococcus pneu	isorder; endocrine disorder; disorder; cancer; human;	
441000000000	22 ABB69159 2 14 AAR38309 3 22 AAU42827 7 22 AAU42827 7 22 AAU42827 6 21 AAG42636 5 19 AAW41166 2 1 AAG42634 1 20 AAY38750 1 20 AAY38751 1 20 AAY38751 2 2 AAB95761 3 22 AAB95761 9 21 AAY51064 9 21 AAY51064 1 22 ABB60669 1 2 AAB60669 2 2 AAB60669 1 2 AAB60669 2 2 AAB60669 1 3 AAR50669 1 3 AAR50669 1 3 AAR50669 1 3 AAR50669 1 3 AAR50669 2 4 AAB6069 2 5 ABB6069 2 5 ABB6069 3 2 5 ABB6069 4 13 AAR50669 6 19 AAW60943	ALIGNMENTS ein; 249 AA. ry) protein. in; hPSP; digestive disorder; immune system n/Qualifiers "signal peptide" "mature hPSP"	S23522. 034429. SCI INC.
22.000.00 2.000.00 2.000.00 2.000.00 2.000.00 2.000.00	6666 6666	(first 1 secret etcry prefersive gnosis. Loca 1 fnot	97WO-U 96US-O GENOME
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1122 1144 1144 1144 1144 1144 1144 1144	1.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	A A WE	XX P XX

Claim 1; Fig 1A-C; 65pp; English.

gastrointestinal tissues

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invention, the property is useful. The UNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immuno effensive, endocrine or immuno system disorders. A particular application is diagnosis of cancers of the salivary gland, through application is diagnosis of cancers of the salivary gland, through application is diagnosis of cancers of the salivary gland, through adjocuted with high levels of hPSP. The protein is also useful as antifungal, antibocterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for the application and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secretory tissue; gastrointestinal tissue; HPSP; Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                             This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and
                                                                                           New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parotid secretory protein; human; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 19; Length 249; 100.0%; Pred. No. 0.091;
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                                                                                                                                                                                                                                            Claim 16; Fig 1; 94pp; English.
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Best Local Similarity Tuv..
5, Conservative
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WPI; 1998-377651/32.
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                                  N-PSDB; AAV44759.
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AAW60682
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that bind specifically to, and modulate activity of HPSP). Antaqonists that bind specifically to, and modulate activity of HPSP are used to treat bind specifically to, and modulate activity of HPSP are used to treat cancer and autorimmune discases particularly or secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, gastrointestinal tract or pancreas, Sjorgen's syndrome, of graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, clerative colitis, Crohn's disease and atrophic gastrilis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may conditionable sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal disorder; glial disorder; astrocytal disorder; anglogenic; phypothalamic disorder; glandilar disorder; macrophagal disorder; epithelial disorder; tromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 51; DB 19; Length 249; 100.0%; Pred, No. 0.091; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO1025 protein sequence SEQ 1D NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24069 standard; Protein; 249 AA.
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99WO-US28313.
99WO-US30911.
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99US-0141037.
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Best Local Similarity 100.0
اندما 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA;
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    The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0290, PR0311, PR0535, PR06109, PR07017, PR08019, PR06191, PR01012, PR01019, PR06191, PR010135, PR010135, PR010162, PR010182, PR010182, PR010187, PR01030, PR010107, PR011011, PR01153, PR01184, PR01187, PR01181, PR01184, PR01187, PR01181, PR01184, PR01181, PR01181, PR01184, PR01181, PR01182, PR01184, PR01181, PR01181, PR01184, PR01181, PR01181, PR01182, PR01184, PR01181, PR01181, PR01184, PR01184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colorectal, prostate, pancratic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalanic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC$8242 to AAC$836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC$8367 to AAC$8367 to AAC$8409 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alizheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                      Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer -
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                                                                                                                                                                   Claim 61; Fig 26; 286pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
Watanabe CK, Wood WI;
                                        WPI; 2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA;
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                                                               N-PSDB; AAC58379
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This sequence represents a human secreted protein amino acid sequence.
The invention relates to sequences AAA87725-A87774 which encode human
Secreted proteins AAB25763-B25812. The proteins include signal peptides.
Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the Secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for accreted proteins. Also contained in the invention are method for storing the sequence data on a computer system, and a method for storing the sequence data on a computer programme.

The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins and applying procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoinfamune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, and informative disorders, grain disorders, diabetes, atheroscierosis, neurodegenerative disorders, gettic tejection, Albrahmer's disease, commentia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                           Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                             Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0141032.
99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                          WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                        mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 dnpghktql 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DNPOHKTOL 9
                                                                                                                                                                                                                                                              N-PSUB; AAA87727
                                                                            (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200100806-A2
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25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Claim 20; Page 260; 1217pp; English.

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                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection \cdot
                                                                                                                                                             The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                       49 Secreted proteins and the nucleic acids encoding them, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 22; Length 249; 100.0%; Pred. No. 0.091;
                                                                                         gene therapy and for detecting similar sequences in samples
                                                                                                                                                                                                                                                                                                                                                  0; Indels
Jobert S;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:1260.
                                                                                                                           Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                       inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 9; Conservative
Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorder.
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                                 WPI; 2001-071487/08.
                                                                                                                                                                                                                                                                                                                                                                                                              237 dnpqhktql 245
                                                                                                                                                                                                                                                         249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        1 DNPQHKTQL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                             . Sequence
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AAM2563. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antinfeummatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardianemic; antianemic; antianemic; antianemic; antianemic; antidabetic; osteopathic; dermatological; antiallergic; antiastummatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; contideration; production. The proteins and polynucleotides are useful for screening for agonitis or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancer, multiple sclerosis, depression, all antiderations and antides ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine influenza virus; ei; cold adaptation; temperature sensitivity; vaccine; neiwtlNP-C-656 DNA; PeiwtlNP-C-217 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine influenza virus H3N8 PeiwtlNP-C-217 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 dnpghktgl 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Claim 5; Page 166-167; 172pp; English.

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Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                  reassortant influence A viruses comprising atleast one genome segment of such an equine influence virus, wherein the equine influence virus, wherein the equine influence virus, wherein the equine influence virus genome segment confers atleast one identifying phenotype of the rold-adapted equine influence virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influence viruses. They are also used as vaccines. The present sequence is equine influence (ei) virus and the virus of virus of the virus of the virus of virus of the virus of virus o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus phenomes segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as
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                  The patent discloses cold-adapted equine influenza viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.5%; Score 37; DB 22; Length 217; 66.7%; Pred. No. 34; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine influenza virus H3N8 PeiwtlNP-C-225 protein.
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//note= "Encoded by AGTTAAAGA"
Misc-difference 224..225
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66...
Best Local Similarity 66...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-522584/57.
                                                                                                                                                                                                                                                                                                              neiwtlNP-C-656 DNA.
                                                                                                                                                                                                                                                                                                                                                                             217 'AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 enpahksql 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
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                                                                                                                                                                                                                                                                                                                                                                                Sednence
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Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV; HCV: digestive disease; Aujeszky's disease virus; pseudorables virus; vaccine; suid herpesvirus 1; swine influenza virus; hog cholera virus; vector; porcline respiratory and reproductive syndrome virus; nucleoprotein; SIRSV: swine infertility and respiratory syndrome virus; nucleoprotein; Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from Aujeskyr's disease virus, swine influence virus (SIV), por concine respiratory and reproductive syndrome virus (PRRSV), hog cholera virus (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. This sequence vas suboloned into the plasmid pVRIO12 to generate plasmid pPB142 for use in the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multi-valent polynucleotide varcines against porcine pathogens consist of at least 3 plasmids able to express protective antigens from specified viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a multivalent vaccine for protecting pigs
cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is equine influenza (ei) virus neiwtln (wild type) NP-C-225 protein which is encoded by neiwtlNP-C-679 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
O
                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 22; Length 225;
66.7%; Pred. No. 35;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 19; Length 498;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW68409 standard; Protein; 498 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIV strain HlN1 nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96FR-0009338.
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swine influenza virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                     225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 enpahksql 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DNPQHKTQL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2751224-A1.
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                                                                                                                                                                                                                                                                         Sequence
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Matches

AAW68407

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The present sequence represents a protein from a Swinepox virus strain an example from the present invention. The present invention specifically describes recombinant swinepox virus (SPV) comprising a foreign DNA (1) inserted into a SPV genome which is capable of being expressed in a host cell into which the virus is introduced, where (1) is inserted into: (a) an ECORI site within a region corresponding to a 3.2 kb subfragment of the Hindlil K fragment which contains both a Hindlil and an ECORI site, of the SPV genome, and optionally (b) an ACCI site within a region corresponding to a 3.6 kb Hindlil to Bgill subfragment of the Hindlil M fragment. The recombinant SPV can be used in a vaccine for immunishing an animal against SPV. The invention also provides a method for testing a swine to determine whether the swine has been vaccinated with the vaccine, particularly containing S-SPV-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   naturally occurring wild-type pseudorables virus. Also (1) inserted into recombinant SPV can be used in a diagnostic assay, e.g. Feline immunodeficiency virus (FIV) env and gag genes and Dirofilaria immits p39 and 22kd are useful to detect feline immunodeficiency caused by FIV and to detect heartworm caused by D. immitis respectively.
                                                                                                             Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis; pseudorables virus; feline immunodeficiency virus; FIV; heartworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PE binding/translocation domains-influenza A virus nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant swine pox virus - useful in vaccine for immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%; Score 37; DB 19; Length 499; 66.7%; Pred. No. 81; Live 2; Mismatches 1; Indels
                                                                   Swinepòx virus Hindill M fragment protein SEQ ID NO:231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 409-410; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR36821 standard; Protein; 917 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal against swine pox virus
                                                                                                                                                                                                                                                                                                                                                    97WO-US12212.
                                                                                                                                                                                                                                                                                                                                                                                                 8969890-S096
                      24-JUL-1998 (first entry)
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochran MD, Junker DE;
                                                                                                                                                              Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYTR ) SYNTRO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-130677/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV26105.
                                                                                                                                                                                                              Swinepox virus.
                                                                                                                                                                                                                                                        WO9804684-A1.
                                                                                                                                                                                                                                                                                                                                                 25-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                            Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV; HCV: digestive disease; Aujeszky's disease virus; pseudorables virus; vaccine; suich herpesvirus 1; swine influenza virus; hog cholera virus; vector; porcine respiratory and reproductive syndrome virus; nucleoprotein; SIRSV; swine infertility and respiratory syndrome virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from Anjeskyl's disease virus, whine influence virus (SIV), portine respiratory and reproductive syndrome virus (PRRSV), hog cholera virus (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. This sequence represents the SIV strain H3NZ nucleoprotein. The coding sequence was subcloned into the plasmid pVRIO12 to generate plasmid pPB132 for use in the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multi-valent polynucleotide vaccines against porcine pathogens consist of at least 3 plasmids able to express protective antigens \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a multivalent vaccine for protecting pigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
    Indels
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2; Mismatches
2; Mismatches
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                                                                                                                                                                                                           AAW68407 standard; Protein; 498 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                      SIV strain H3N2 nucleoprotein.
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    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from specified viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swine influenza virus.
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                                                                                           320 enpahksql 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV49301.
                                               1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR2751224-A1.
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Gaps

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RESULT 11

AAW55986

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nucleoprotein; NP; PCR; amplification; translocation; binding; domain.
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                                                                                                                                                                    Montgomery DL, Oliff Al,
                                                                                                                                  (MERI ) MERCK & CO INC.
                                                                                                                                                                                            WPI; 1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 enpahksgl 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                        N-PSDB; AAQ38411
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                                                                                                          09-SEP-1991;
                                                                                   02-SEP-1992;
                                                                                                                                                         Donnelly JJ,
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                                                              17-MAR-1993
                                    EP532090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful as vaccines against viral infections, tumours and
                                                                                             /note- "amino acids 2-414 of PE domains 1 and II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE binding and translocation domains - Influenza A nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVC-PENPcSaa; pApr501; pBR322; pVC-PEMI-2;
Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; NP; anti-viral agent; Pseudomonas exotoxin; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 37; DB 14; Length 917; 66.7%; Pred. No. 1.5e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      Hawe LA, Liu MA, Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pApr501 was constructed from the influenza A virus
                                                                                                          /note- "influenza A virus Nucleoprotein"
913..917
                                                                                                                                            /note= "last 5 amino acids of PE"
                                                                                                                                                                                                                                                                                                   Shi X, Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                        Example 25; Page 63-67; 81pp; English.
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR32469 standard; Protein; 917 AA.
                                      Chimeric Pseudomonas aeruginosa.
                                                                                                                                                                                                                 92EP-0310067.
                                                                                                                                                                                                                                         91US-0792507
                                                 Chimeric Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                       Friedman A,
                                                                                                                                                                                                                                                                                                   Montgomery DL, Oliff AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                         415..912
                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                        WPI; 1993-154266/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 enpahksgl 742
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                                                                                                                                                                                                                  04-NOV-1992;
                                                                                                                                                                                                                                          08-NOV-1991;
                                                                                                                                                                                                                                                                                      Donnelly JJ,
                                                                                                                                                                                          12-MAY-1993
                                                                                                                                                                   EP541335-A.
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Example 25 describes the construction of pvC-PENPcSaa. A fragment contg. the nucleoprotein (NP) of Influenza A virus was obtained from plasmid pApr501. pApr501 is the nucleoprotein gene cloned into the EcoRI site of pR8222, by PCR with oligonucleotide primers which added a SacII site adjacent to the ATG codon of NP to give the sequence of AAQ38409, and the last 5 amino acids of PR followed by a termination codon and an EcoRI site to the 3' end of NP to give the sequence shown in AAQ38410. The PCR fragment was digested with SacII and EcoRI. The resulting plasmid pVC-PEMI-2 digested with SacII and EcoRI. The resulting plasmid is named pVC-PENPCSEAB. The S' and 3' ends of the PRNPSaa insert (AAQ38411) were verlified by sequencing. This construction fuses the binding and translocation domains of PE to the Influenza A nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli proliferation associated protein sequence SEQ ID NO:301.
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                                                                                                                                                                                                                                                               , Liu MA, Marshall MS;
Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 66-70; 85pp; English.
                                                                                                                                                                                                                                                               Friedman A, Hawe LA,
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92EP-0202660
                                                                                   91US-0756249
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Gaps

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Disclosure; Fig 3; 228pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAA66055 and AAB15806 to AAB16040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to indicate a proliferation inhibiting nucleotide done in a microorganism, by contacting a microorganism with a proliferation-required gene in a microorganism, by contacting nucleic acid identified in another organism, and determining if nihibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                        Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a virulence factor encoded by ORF14991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pathogen; virulence polypeptide; virulence factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenic infection; Pseudomonas aeruginosa infection.
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Pred. No.
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Rahme LG, Tan M, Tsongalis J;
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85.7%;
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99US-0117405
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                                                       (ELIT-) ELITRA PHARM INC
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Best Local Similarity
6; Conserva
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                                                                                                                                      Xu HH;
                                                                                                                                                                                          WPI; 2000-514822/46.
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  27-JAN-1999;
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                                                                                                                                      (amamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1997;
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                                                                                                           Zyskind J,
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TAAY29160
TAAY29160
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AAY20
AAY2
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The present sequence represents a Pseudomonas aeruginosa polypeptide sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                     note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not entirely correct.
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Sequence 16, Appl
Sequence 16, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 16, Appli
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Sequence 14, Appl
Sequence 14, Appl
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Sequence 3, Appli
Sequence 4, Appli
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Sequence 24, Appl
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                                                                                                        August 6, 2002, 16:53:56; Search time 51.22 Seconds (without alignments) 4.292 Million cell updates/sec
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Sequence 4,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/GCOMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-232-468A-24
US-08-068-968C-231
US-09-199-637A-229
US-08-102-863-11
PCT-0852-1085-11
US-08-107-858-14
US-08-107-858-14
US-08-107-858-14
US-08-107-858-14
US-08-107-858-14
US-08-107-858-14
US-08-147-068A-2
US-08-474-067-2
US-08-474-068A-2
US-08-474-068A-5
US-08-474-068A-4
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US-08-781-890-16
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PCT-US96-03180-16
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51
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 7,
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Sequence 18, Application US/09232468A
Sequence 18, Application US/09232468A
Sequence 18, Application US/09232468A
SERENT NO. 6207165
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2330
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOS: 2.1
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Sequence 24, Application US/09232468A
Patent No. 6207165
GENERAL INFORMATION:
APPLICANT: AUDONNE et al.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
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          US-08-729-834B-5
US-09-300-681B-4
US-09-300-681B-4
US-09-300-681B-2
US-09-284 0.33-2
US-09-284 0.33-2
US-08-729-834B-2
US-08-729-834B-2
US-08-765-081-6
US-08-765-081-6
US-09-098-082-6
PCT-US-055-0693-7
US-09-093-7
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US-09-087-465-10
US-07-797-556-6
US-07-943-843-2
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CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: swine influenza virus US-09-232-468A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: swine influenza virus US-09-232-468A-24
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Best Local Similarity 66.7'
Matches 6; Conservative
 1126
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70.6%; Score 36; DB 4; Length 132;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 0; Indels
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                     1; Indels
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APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Manajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                          APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOOTWARE: PatentIn Ver. 2.1
SEQ ID NO 231
LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
66.7%; Pred. No. 27;
tive 2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION UNBER: 60/066,517
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                   Sequence 231, Application US/08686968C; Patent No. 6221361; GENERAL INFORMATION: APPLICANT: Cochran, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%
    Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Swinepox virus
US-08-686-968C-231
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320 ENPAHKSQL 328
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US-08-686-968C-231
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GENERAL INFORMATION:
APPLICANT: SARIASLANI, SIMA
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                 CONSTITUTIVE
EXPRESSION OF P450SOY
AND FERREDOXIN-SOY IN
STREPTOMYCES
                                                                                             APPLICANT: SARIASLANI, SIMA
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SO
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
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ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CSOFTWARE: Version #1.25 CSOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/102.863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   Sequence 11, Application US/U8102863
Patent No. 5466590
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                         1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 302-892-7949
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                                                                                                                                                                                                                                                                                                                                                                    19898
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PCT-US92-10885-11
RESULT 5
US-08-102-863-11
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ORGANISM: Arabidopsis thaliana US-09-107-858-14
               INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 345 amino acids
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Win
                                                       : 345 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
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Matches 5; Conservative
(617)227-5941
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Matches 5; Conservative
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                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-758-621-14
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ZIP: 19406-0939
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| 110 DNPRHK 115
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   TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                        SYSTEM: Macintosh System, 6.0
Microsoft Word, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REGISENCE/DOCKET NUMBER: DCI-099CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                 UMBER: PCT/US92/10885
19921216
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                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/POCKET NUMBER: CF
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INFORMATION FOR SEQ ID NO: 11:
     : 1007 MARKET STREET
WILMINGTON
DELAWAKE
                                                                                                                                                                                                                                                                                                                                                                            302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: AMINO ACID
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Best Local Similarity 62.59
Matches .5, Conservative
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APPLICATION NUMBER: PC1
FILING DATE: 19921216
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OPERATING SYSTEM: MA
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ZIP: 02109-1875
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                                                                               19898
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                                                                   COUNTRY:
                                           STATE:
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64.7%; Score 33; DB 2; Length 345; 83.3%; Pred. No. 97; tive 1; Mismatches 0; Indels
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APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
APPLICANT: Stodola, Robert
NITLE OF INVENTION: 00. 6348328el Compounds
NUMBER OF SEQUENCES: 552
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FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 318, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
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NOVEL PROTEIN HAVING NITRILE HYDRATASE
ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR F
FROM NITRILES VIA A TRANSFORMANT CONTAINING THE GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
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TITLE OF INVENTION: NOVEL PROTEIN
TITLE OF INVENTION: ACTIVITY AND I
TITLE OF INVENTION: FROM NITHILES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELEVANT RESIDUES IN SEQ ID NO: US-08-052-681-3
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Patent No. 5314819
GENERAL INFORMATION:
                                                                                                                                                                                                  STRAIN: Rhizobium sp. MC12643
115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD:
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PUBLICATION INFORMATION:
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                                      STRANDEDNESS: single
                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                   INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMUSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: No.
                   TYPE: amino acid
                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION DATE:
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IMMEDIATE SOURCE:
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                                                                                                  HYPOTHE'LICAL:
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LOCATION:
                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL:
                                                                                                                       ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
    LENGTH:
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PAGES:
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TITLE OF INVENTION: NOVEL PROTEIN HAVING NITRILE HYDRATASE
TITLE OF INVENTION: ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR PROG
TITLE OF INVENTION: FROM NITRILES VIA A TRANSFORMANT CONTAINING THE GENE
NUMBER OF SEQUENCES: 14
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                 UMBER: US/08/858,207A
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/052,681
                   CARGE APPLICATION UNMER: US/08/858,20
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTONREY, AGENT INFORMATION:
NAME: Gimmi, Fdward R
REGISTRATION NUMBER: 38,891
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APPLICATION DATA:
APPLICATION NUMBER: US/NP.//
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 318:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
MOLECULE TYPE: No. 6348328e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202-371-8850
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                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19930427
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                        single
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US-08-474-067-2
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62.7%; Score 32; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,681
FILING DATE: 1930427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium sp. MC12643
                                                                                                                                                                                                              NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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PUBLICATION INFORMATION:
                                                                                             FILING DATE: 19930427
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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MAP POSITION:
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LIBRARY:
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ORIGINAL SOURCE:
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78 DNPQH 82

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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474.067
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Ranscht, Barbara
APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                     APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A.
RECISTRATION NUMBER: 315
REFERENCE/DOCKET NUMBER: P-LJ 1682
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5811518
Sequence 2, Application US/08474067; Patent No. 5811518
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 712 amino acids
amino acid
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Best Local Similarity 100.0
These 6; Conservative
                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 92122
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
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STATE: California
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APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,068A FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                     PRIORA APPLICATION 1974

PRIORA APPLICATION 1974

FILIND DATE: 14-MAY-1994

PRIORA PAPLICATION NUMBER: US 07/607,293

PRIORA APPLICATION NUMBER: US 07/607,293

PILING DATE: 30-007-1990

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 1682

REFERENCE/DOCKET NUMBER: P-LJ 1682

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/213,361
FILING DATE: 14 MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-0CT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                       APPLICATION NUMBER: US/08/474,067 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08474068A
; Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-I TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 712 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-474-067-5
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                                                                                                                     FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Cali
COUNTRY: Un
ZIP: 92122
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2 QHKTQL 7
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US-08-474-068A-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.7%; Score 32; DB 2; Le Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                   Query Match 62.7%; Score 32; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6: Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPELICATION NUMBER: US/08/474,068A PAPELICATION NUMBER: US/08/474,068A FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTOKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P-LJ 1683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/08474068A
; Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 712 amino acids
amino acid
GY: linear
                                                             : 712 amino acids
amino acid
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                                                                                                                         , MOLECULE TYPE: protein US-08-474-068A-2
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                         linear
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Search completed: August 6, 2002, 16:53:57 Job time: 289 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 6, 2002, 16:52:58 ; Search time 32.88 Seconds (without alignments) 293.223 Million cell updates/sec

US-10-020-139-2 Title: Perfect score: Sequence:

1 MLQLWKLVLLCGVLTGTSES........NV1QQVVDNPQHKTQLQTLI 249

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 105224 segs, 38719550 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		2 2 2	Ĕ		_		_	P16154 clostridium		haem	_	tomato	tomato	sacchar	Ŋ			Sa	E		buchnera	saccharon	S			tomat	haemophil		C	a a		listo	ccharon
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P16573	00120	049460	009793	058556	09v7a4	P12612	010339	063313	09usi6	P46939	P4 9022
ECTO_RAT	METE_AQUAE	Y468_MYCGE	NG79_SCHPO	YB56_METJA	ITA4_DROME	TCPA_YEAST	YBM2_SCHPO	LBP_RAT	MYS2_SCHPO	UTRO_HUMAN	PIP_LACLA
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90.5	90.5	90.5	06	06	06	89.5	89.5	68	68	8	88.5

# ALIGNMENTS

15 S A .	STANDARD;  (Rel. 08, Cree (Rel. 08, Last etory protein (Mouse). etazoa; Chorda theria; Rodent 0090; M.A. id gland; 5456; Pubmed-2 10010g of mous 1-87 FROM N.A. TISSUE-Spleen; 4556; Pubmed-2 4556; Pubmed-2 1-87 FROM N.A. TISSUE-Spleen; 7550 FROM N.A. TISSUE-Spleen; 7570 FROM N.A. TISSUE-Spleen; 7570 FROM N.A. TISSUE-Spleen; 7570 FROM N.A. TISSUE-Spleen; 7570 FROM N.A. TOF SALIVARY
 DR EMBL; XO, DR EMBL; MZO DR PIR; A230 DR PIR; A230 DR POD; MGI KW PATOLIG G FT CHAIN SQ SEQUENCE	EMBL, X01697; CAAA2846.1; - EMBL, M26807; AAA40009.1; - EMBL, M26806; AAA40009.1; JOINED. EMBL, M26806; AAA40009.1; JOINED. EMBL, M26806; AAA40009.1; JOINED. EMBL, M26806; AAA40009.1; JOINED. EMBL, M26806; AAA7844009.1; JOINED. EMBL, M2787, PROTEIN. SEQUENCE 235 AA; 24753 MW; 23311BARIEGEZEF3 CRC64;
Ouery Match Best Local Similarity Matches 81; Conser	29.6%; Score 364.5; DB 1; Length 235; imilarity 33.8%; Pred. No. 2.1e-20; Conservative 62; Mismatches 80; Indels 17; Gaps 3;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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MEDLINE-99240770; PubMed-10224143;
MESTON W.M., LeClair E.B., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
"Differential display identification of plune, a novel gene expressed in embryonic palate, nasal epithellum, and adult lung.";
1. Biol. Chem. 274:13698-13703(1999).
                                                                                                                                                                                                                                                                                                                                         106 NGNGIDLTVPLAGGASLVLPPIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGKCSSNT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 DKISJSLLGRRLPIINSLLDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSVLQGLLSN 225
                                                                                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSLILDVKAEPID 118
                                                                                                                                                                                                                  49 DVELLQQATSWPLAKNSILET --- LNTADLCNLKSFTSLNGLLLKINNLKVLDFQAKLSS 105
                                                                                                                                                                                                                                                                                                 119 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TSISLSLLDKHSOIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 238
                                           1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization of the mouse plunc gene and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  weston W.M., LeClair E.E., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
J. Biol. Chem. 275:8565-8562(2000).
-!- FUNCTION: May be involved in the airway inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     after exposure to irritants. May be associated with tumor progression (By similarity).

-- SUBCELLULAR LOCATION: Secreted (By similarity).

-- TISSUE SPECIFICITY: Upper airways, nasopharyngeal regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeClair E.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 284:792-797(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21290678; PubMed=11396972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBĽ; AF356785; AAK63069.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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138 PIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLLDKHSGIINK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SPALPSNPTDLLAGKFTDALSGGL-----LSGGL-----LG1LENIPLLDVIKSGGN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AEKLLNNVISKL---LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein Plunc precursor (Palate lung and nasal epithelium clone protein) (Lung specific X protein) (Nasopharyngeal carcinoma-related protein) (Tracheal epithelium enriched protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFLVGSLVVLCGLLAHSTAQLAGLPLPLGQGPPLPLNQGPPLPLNUGQLLPLAOGLPLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 ----SNVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQE 80
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                                                                  4 X 6 AA KEPEATS OF G-[LPU]-[PL]-L-P-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bingle C.D., Bingle L.; "Characterization of the human plunc gene, a gene product with an upper alrways and nasopharyngeal restricted expression pattern."; Biochim. Biophys. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                N-LINKED (GLCNAG. . .) (POFENTIAL)
N-LINKED (GLCNAG. . .) (POFENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He 2.W., Yao K.T., Xu L.G., Ren C.P., Lan K., Xie L., Zhang L., Liu W.D., Zhou W., Wang L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 :
                                                                                                                                                                                                                                                                                                                                                                                              15.8%; Score 194.5; DB 1; Length 278; 23.5%; Pred, No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 FVDNLTGILTKYLPELIQGKVCPLVNGILSGLDVTLVHNIAELLIHGLQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                  7F40BED9859188FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLQLWKLVLLCGVLTGTSESLLD-------NLGNDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09NP55; 09NZT0;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA
                                   PROTEIN PLUNC
   POTENTIAL
                                                                                                                                     REPEAT 2
                                                                                                                                                                                                    REPEAT 4
                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20472055; PubMed-11018263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21150203; PubMed=11251963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Cancer 91:433-437(2001).
278 PPC 278 PPC 278 PPC 28 PPC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23.5%
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_Tax LD=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLUNC OR LUNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ung cancer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLUN_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                      CHAIN
                                                                                                                              REPEAT
REPEAT
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RA JOURNEE FROM N.A.

RA JOURNAE P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA JORES M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Buck D., Burrill W., Buler A.P., Carder C. Carter N.P.,

RA Coulson A., Coville R.E., Connor R., Carter N.P.,

RA Coulson A., Coville R.E., Connor R., Corby N.R.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.

RA Fafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE_21317946; pubmed-11425234; Lindahl M. Stahlbom B. Tagesson C.; Indahl M. Stahlbom B. Tagesson C.; Indahl M. Stahlbom B. Tagesson C.; Indahlication of a new potential airway irritation marker, palate two-dimensional epithelial clone protein, in human nasal lavage fluid with elescription/ionization-time of flight. ... Electrophoresis and matrix-assisted laser electrophoresis 22:1795-1800(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: Upper airways and nasopharyngeal regions, including trachea and nasal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor
"Cioning a new gene related to nasopharyngeal carcinoma.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN PLUNC,
Q -> K (IN REF. 1; AAF70860).
EDF152FBC35315BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 95-152; 157-167 AND 214-232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and some other types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         progression.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF214562; AAG13653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB024037; BAA93633.1;
IMBL, AF158745, AAF92622.1;
EMBL, AL121901; CAC03549.1;
EMBL; BC012549; AAH12549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF70860.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 256 F
220 220 6
256 AA; 26712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE~Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
CONFLICT
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SIGNAL
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             14.9%; Score 183.5; DB 1; Length 256;
23.8%; Pred. No. 7e-07;
Live 46; Mismatches 100; Indels 33; Gaps
                                                                                                                      75 KOKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                             132 NVTVAGPIIG-OIINLKASLDLLTAVTIETDPOTHQPVAVLGECASDPTSISLLDKHS 190
                                                                                                                                                                                                         138 KLQVNTPLVGASLLRLAVKLDITAEILAVRDKOERIHL-VLGDCTHSPGSLQISLLDGLG 196
                                                                15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                           "A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar Yeast 11:873-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 SILTFLDKEDKPVCDKFITSYTRSIARYDRS-----KLNIILSLLKK-----IRLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 SLLDNLGNDLSNVVDKI.EPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 79
                                                                                                                                                                                                                                      191 QI-INKFVNSVINTLKSTVSSLLOKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetiaes; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 200.0 kba protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 109; DB 1; Length 1769; 19.2%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             064480D1D249B241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C / FY1679;
MEDLINE=96090136; Pubmed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 249384; CAA89404.1;
SGD; S0003645; YJL109C,
InterPro; IPR00357; HEAT_repeat.
PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200080 MW;
Query Match
Best Local Similarity 23.8%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X85021; CAA59385.1; -.
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1769 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen S.W.;
                                                                                                                                                                                                                                                                                                                                         YJK9_YEAST
P42945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                          YJK9_YEAST
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                                                                                                                                        191 QIIN------KFVNSVINTLKSTVSSLLQKEICP 218
                                                                                                                                                                 ::I | :: | | :: | | 474 ELINTINVSMLTETGERYKKVLSLFTEAIGKGYKASSFLTSFFTTLESRITFLLRVTISP 533
80 EAEKLLNNV1--SKLLPTNTD1----FGLKISNSI,ILDVKAEPIDDGKGLNLSFPVTAN 132
                              379 EVRLITTDLIYLSEILEDKSQLVELFEYFISINEDLVLKCL------KSLGLT----- 425
                                                                    133 VTVAGPIIGQIINLKASLDLLTAVTIETD - PQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                    426 -----GELFEIRLTTSLFTNADVNTDIVKQLSDPV----ETTKKDTASFQTFLDKHS 473
                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. BACKETIOL. 175:7485-7489(1993).

-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate - glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
-!- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHIFF-BASE WITH DIHYDROXYACETONE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
A189E75574F1FCC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S33358; S33358.

PIR; A49943; A49943.

HSSP; P14223: 1A5C.

HSSP; P14223: 1A5C.

Pfam; PF00274; glycolytic_enzy; 1.

ProDom: P0001128; Aldolase_I: 1.

ProSTIE: P800158; ALDOLASE_CLASS_I; FALSE_NEC.

Lyage: Schiff base: Glycolysis.
                                                                                                                                                                                                                  219 LIRIFIHSLDVNVIQQVVDNPQHKTQLQTL1 249
                                                                                                                                                                                                                                       Bacteriol. 175:7495-7499(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94042930; PubMed-8226699;
Kula M.R., Brockamp H.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=TM300;
MEDLINE=94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 AA; 32720 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus carnosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witke C., Goetz F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witke C., Goetz F.;
J. Bacteriol. 175:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carnosus."
                                                                                                                                                                                                                                                                                                                                                 ALF_STACA
007159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jimenez M., Petit T., Gancedo C., Goday C., The alm1+ gene from Schlzosaccharomyces pombe encodes a colled-coil protein that associates with the medial region during mitosis.";
                                                                         52 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKILINNVISKILPTNTDIFGLKISNSLILD 111
                                                                                                                                                                                                                               152 -----LLTAVTIET------DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKF 196
                                                                                                                                                                                                                                                      203 KKDQYVMLKIJIDTKVNAYSELJEHPQVIRVVALSGGYSKDEAN---KILKQNIXJIASF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   145 NNKEAIE--KVVKQQFEVAKEIIAAGLVPIIEFEVNINAKDKEAIEANIAEAIKAELJNL 202
                                                                                                              93 KGIVPFLKVDKGLAEEADGVQLMK-PIPDLDKLI,DKA-----NEKGIFGTKM-KSNILE 144
                                         64; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,
CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of GFP-gene fusion library of fission
Ouery Match
Best Local Similarity 25.9%; Pred. No. 0.5;
Matches 50; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OUTES: 013313; Q9UTT8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Abnormal long morphology protein 1 (Sp8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1727 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL133357; CAB62414.1; -.
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                        260 SRALVSDLNAQOS 272
                                                                                                                                                                                                                                                                                                                 197 VNSVINTLKSTVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-968 H90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOKINESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ding D.;
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                                                                                                                                                                                                                                   333 SENSIRELQEKYDSVVSELOVVKENKNTSVSAGVGLFSPLAOKLSAVQNPEFSFTKVYSD 392
                                                                                                                                                                                                                                                                50 --TLKGILEKLKVDI.GVLQK--SSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIF 100
                                                                                                                                                                                                                                                                                         393 NMKLQOKVSSLKLOLDKLTNKFSSFCEQVKORIPVVKOORSEIVRNNIYMNFLSES---- 448
                                                                                                                                                                                                                                                                                                                    101 GLKISNSLILUVKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 159
                                                                                                                                                                                                                                                                                                                                                                         160 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 219
                                                                                                                                                                                                                                                                                                                                               449 - LETSNNNLTKVQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSR 507
                                                                                                                                                                                                         18 SESLLDNLGNDLSNVVDKLEPV-------49
                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton K.A., Fleischmann R.D., Bult. G.J., Kerlavage A.R., Sulton G., Kolley J.M., Britchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Tomb J.-F., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Peterson S.N., Smith H.O., Hutchison C.A., III, Venter T.S., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                 61;
                                                                                                                                                                  DB 1; Length 1727;
                COLLED COIL (POTENTIAL).
3 MW; F820BF8D9C132644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                          94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYTACHTON: 175:7918-7930(1993).
-!- FUNCTION: COULD BE A ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P200_MYCGE STANDARD; PRT; 1616 AA. 049429; C49259; C49298; C49353; 01-NOV-1997 (Rel. 35, Created) STANDARD; C1-NOV-1997 (Rel. 35, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                         8.5%; Score 104.5; L
24.3%; Pred. No. 6.4;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; Pubmed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94075230; Pubmed=8253680;
                                                                                                                 197858
                                                                                                                                                                        24.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 LREKVRALECDVEIQKOTV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                  220 IRIFIHSL--DVNVIQQVV 236
                                                                                                                                                               Best Local Similarity 24.39
Matches 63; Conservative
                                            740
1106
1427
1555
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                                                                                                              1727 AA;
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Coiled coil.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      461 SKEIKDSAKADLSNISDDIDSVWKEFGSFTDETQKSVEEKSQVDEIILDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQOEFSEPVVSDEKIKETNSDESVNTDL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 -~IFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQI--IN---- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 TALESEKLVNEVLL -- TNEYUD----VNAPFSTETEVKVSSELPKSELVDEITFINNDPK 631
                                                                                                                                                                                                                                                                                                                                                                              18 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ----LKASLDLL------TAVTIETDPQTHQPVAVL------GECASDPTSI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 PQEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDI,SLELNSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLJRIFIHSLDVNVIQQVVDNPQH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- KLLPTNTD----- 98
                                                                                                                                                                                                                                                                                                                                                               75; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                         Structural protein; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                               8.4%; Score 104; DB 1; Length 1616;
20.6%; Pred. No. 6.4;
tive 48; Mismatches 75; Indels 12
                                                                                                                                                                                                                                                                                   > F (IN REF, 2).
6AF76A13AC49E4FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-VPI 10463;
MEDLINE-90221894; PubMed-2109310;
Sauerborn M., von Elchel-Streiber C.;
Nucleotide sequence of Clostridium difficile toxin A.";
                                                                                                                                                                                                                                                                     P -> S (IN REF. 2).
S -> F (IN REF. 2).
                                                                                                                                                                                                                                  2 X 26 AA REPEAT.
                                                                                                                                                                                            2 X 32 AA REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                  EMBL; U02245; AAA03401.1; ALT_FRAME.
EMBL; U02175; AAD12458.1; -.
EMBL; U02126; AAD12402.1; -.
                                                                                                                                                                                                                                                                                              185678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AQEAEKLLNNVIS------
                                                                                        EMBL; U39720; AAC71613.1; -.
                                                                                                        EMBL; U02245; AAA03400.1; -
                                                                                                                                                                                                                                                                                                                                                       63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium difficile.
                                                                                                                                                                                                                                                                                          1616 AA;
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1310
256
304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 KTQLQT 247
                                                                                                                                                                      Cytadherence;
                                                                                                                                                           MG386;
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phases of the cell cycle.
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                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          674 67
1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLY PROPHASE)
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                 NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364
737
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                                                       KNSL,1 OR EGS.
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NP_BIND
MOD_RES
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STEETE TEETER AND SHARE THE TEETER AND THE TEETER A
                                                                                                                                                                                                                                                                                                                                                                                                                                   this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 IIKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 TIETDPOTHOPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 57
                                                                                                                                                                                                                                "Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 104; DB 1; Length 2710; 20.3%; Pred. No. 12;
                                                                                        Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match
Local Similarity 20.3%; Pred. No. 14;
Local Similarity 63; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EG5. HUMAN STANDARD: PRT; 1057 AA. P52332; 015716; 01-0cT-1996 (Rel. 34, Created) 01-0cT-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 249
  Nucleic Acids Res. 18:1629-1630(1990).
                                                             STRAIN=VPI 10463;
MEDLINE=90129305; Pubmed=2105276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002479; CW_binding.
Pfam; PF01473; CW_binding_1; 31.
Toxin; Enterotoxin.
                                                                                                                                                                        infect. 1mmun. 58:480-488(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X51797; CAA36094.1; -. EMBL; M30307; AAA23283.1; -. EMBL; X92982; CAA63564.1; -. PTR; S08638; S08638.
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
EG5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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Kinesin-related motor protein Eg5 (Kinesin-like spindle protein HKSP)
(Thyroid receptor interacting protein 5) (TKHP5) (Kinesin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOI. Endocrinol. 9:243-254(1995).

-!- FUNCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIFOLAR SPINDLE. BLOCKING OF EGS PREVENTS CENTROSOME MIGHATION AND ARREST CELLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS.

-!- SUBUNIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE
                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96128120; PUDMEd-8548803; MEDLINE-927, AND MUTAGENESIS. MEDLINE-96128120; PubMed-8548803; Mlarin P., Harper M., Kress M., Nigu E.A.; Blangy A., Lane H.A., D'Herin P., Harper M., Kress M., Nigu E.A.; "Phosphorylation by p34cds regulates spindle association of human "phosphorylation by p34cds regulates spindle association of human by5, a kinesin-related motor essential for bipolar spindle formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92295737: PubMed-7776974;
Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.:
"Two classes of proteins dependent on either the presence or absence
of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
PHOSPHORYLATION (BY CDC2).
T->A: NO MITOTIC PHOSPHORYLATION. NO
BINDING TO SPINDLE APPARATUS.
                                                                                                                                                                                                      Eŭkaryola, Metazoa, Chordata, Craniata, Vertebrata, Euteleustumi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitehead C.M., Rattner J.B.; Expanding the role of Publication Expanding the role of Heggs within the mitotic and publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Microtubules; ATP-binding; Coiled coil; Mitosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E322F2141BEF1601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98369052; PubMed-9701554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell Sci. 111:255i-2561(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; 1PR001752; kinesin.
Pfam; PF00225; kinesin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 819-868 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER LINKAGES BETWEEN 5'-PHOSPHORYL AND 3'-HYDROXYL GROUPS IN DOUBLE-STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF DAMAGED DNA (BY SIMILARITY).

--- CATALYTIC ACTIVITY: NAD(+) + (deoxyribonucleotide)(N) + (deoxyribonucleotide)(M) = AMP + nicotinamide nucleotide + (deoxyribonucleotide)(M) = AMP + nicotinamide nucleotide + 1 SIMILARITY: BELONGS TO THE NAD.DEPENDENT DNA LIGASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             494 DAASKLLNTVEE----TTKDVSGLHSKLDRKKAVDQHNAEAQDJFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                                                                                                     550 KDGSSKQKAMLEVHKTLFGNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                                                                                                                                                                                                   182 SLSLLDKHSQ1INKF------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=RD, KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MELSCHMARD R.D., Adams W.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hannam M.C., Nguyen D.T., Sauddek D.M., Brandon K.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                            79; Indels 70; Gaps
                                                                                                                                447 LDQCKSDLQNKTQELE-----TTQKHLQETKLQL-VKEEYITSALESTEEKLH 493
                                                                                                                                                                            80 E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 127
                                                                                        22 LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKI,KVDLGVLQK··SSAWQLAKQKAQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
                                                                                                                                                                                                                                                                128 ----PVTANVTVAGPIIGQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
8.1%; Score 100; DB 1; Length 1057; Similarity 24.4%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.^{-};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 AA
                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGN OR LIG OR HI1100.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=727;
             Local Sim.
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                            229 VN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 IN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNLJ_HAEIN
P43813;
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNLJ_HAEIN
                                                Matches
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RRPO_TOWK2 STANDARD; PRT; 1616 AA.
P89676. p90349;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Methyltransferase/RNA helicase (EC 2.7.7.48) (183 KDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)].
Tomato mosalc virus (strain Kazakh K2) (TOWY) (TWY strain K2).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOIL BIOI. (MOSK) 31:826-830(1997).
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL RNA REPLICATION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA -!- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 KLLNNV------ISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ANVIVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 VVIRRAGDVIPOII------GVLHERRPDNAKPIIF-----PINCPVC----DS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 SLGYDIDGTVLKINDI-------ALQNELGFISKAPRWAIAYKFPAQEEL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 NLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA-KQKAQEAE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 QIINKEVNSVINTLKSTVSSLLQKEICPLIRIFI--HSLDVN-----VIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K.; "Properties and structure of the tobacco mosaic virus strain K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligase; DNA repair; DNA replication; NAD; Complete proteome. DOMAIN 601 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 99; DB 1; Length 679;
23.1%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.1%; Prec. ....
Watches 54; Conservative 41; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                            DNA_ligase_OB.
DNA_ligase_2BD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50172; BRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
PROSITE; PS01056; DNA_LIGASE_N2; 1.
                                                                                                                                                                                                                                                                                                                                                                 PD003944; DNA_ligase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-9854068;
                                                                                                                                    DNA_ligase_N.
                                                                                                                                                                                                                                                Pfam: PF00533; BRCT; 1.
Pfam: PF01653; DNA_1igase_N; 1.
Pfam: PF03120; DNA_1igase_OB; 1.
Pfam: PF03119; DNA_1igase_ZBD; 1.
Pfam: PF00633; HHH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679 AA; 75188 MW;
                                                EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                     InterPro; IPR000445; HHH.
InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00532; LIGANC; 1.
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00292; BRCT; 1.
SMART; SM00278; HhH1; 2.
                                                                                                                 InterPro; IPR001357;
InterPro; IPR001679;
                                                                                                                                                            InterPro; IPR004150;
                                                                                                                                                                                  InterPro; IPR004149;
                                                                        1B04.
                                                                     087703;
                                                                                             HI1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                    ProDom;
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EMBL; X02144; CAA26085.1; -.
                                                                                                                                                       EMBL; X02144; CAA26082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 20.49
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                               1616
1116
                                                                                                                                                                      PIR; A04195; WMTM8T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                             NP_BIND
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                                                                                                                                                     RRPO_TOML STANDARD: PRT; 1616 AA.
P03587: 041352;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-NA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)].
Tomato mosalc virus (strain L) (TOMY) (TMV strain tomato).
Viruses; ssrNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 1DDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 MTAAKVIVAVMSNESGLTLLTFEQPTEANVALA-----LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·! - FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPPING AND AN RNA HELICASE.
-!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
-!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                           Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and comparison with the common strain genome."; J. Biochem. 96:1915-1923(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohno T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                         METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                          C2F5CE0C8C965336 CRC64;
                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 98.5; 20.4%; Pred. No. 16
                                                                                                                                                                                 EMBI. 292909: CABO7438.1;
InterPro: IPR001708; RNA_dep_RNApol2.
InterPro: IPR001708; V_methyltransf.
InterPro: IPR002606; Viral_helicasel.
Pfam: PF00978; RNA_dep_RNApol2; 1.
Pfam: PF001443; Viral_helicasel.
Pfam: PF01660; Vmethyltransf: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85157522; PubMed=6549393;
                                                                                                                                                                                                                                                                                                                                          833 840 ATE
1616 AA; 183614 MW;
                                                                                                                                                                    EMBL; 292909; CAB07439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 YTGPLKVQQMKNF1DS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12252
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                               Ogykb6, Ogwu37;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein) (Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSL11.DVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLOKEICPLIRI 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou X., Xue C., Chen Q., Qi Y., Li D.; "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato mosaic virus (strain S-1) (TOMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TaxID=138314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPPING AND AN RNA HELICASE.
MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; PF01660; Vmethyltransf; 1.
Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 98.5; DB 1; Length 1616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
Pfam; PF00978; RNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicasel; 1.
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1616 AA; 183564 MW;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288C / FY23;
MEDLINE=96405918; Pubmed=8810043;
Miosga T., Zimmermann F.K.;
Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR";
                                                                                                                                                                                                                                                                                                                                                                                                                                      57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                 117 IDDGK-----GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 164
                                                                                                                                                                                                                                                                                                                                                                                                                      165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 222
                                                                                                                                                                                                                                                                                          44; Mismatches 79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gammie A.E., Kurihara L.J., Vallee R.B., Rose M.D.;
"DNM1, a dynamin-related gene, participates in endosomal trafficking
                                                                                                                                  Interpros irrovovovo
Pfam: PF00978: RNA-dep_RNApol2: 1.
Pfam: PF01443: Viral_helicase1: 1.
Pfam: PF01660: Vmethyl.transf: 1.
Transferase: RNA-directed RNA polymerase: Helicase: ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                  DB 1; Length 1616;
                                                                                                                                                                                                                  ATP (POTENTIAL).

IN: 5DBBFB2FADCC5C0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNMIOR YLL001W OR 1.1381.
                                                                                                                                                                                                                                                                 Match 8.0%; Score 98.5; 1 Local Similarity 20.4%; Pred. No. 16;
                                                                                                    InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=S288C;
MEDLINE=95348179; PubMed=7622557;
                                                                                                                                                                                                                 833 840 ATP
1616 AA; 183542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 130:553-566(1995).
                                                                            EMBL; AJ132845; CAB36997.1; -. EMBL; AJ132845; CAB36998.1; -.
                                                                                                                                                                                                                                                                                            40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 YTGPLKVOOMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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P54861;
                                                                                                                                                                                                                  NP_BIND
SEOUENCE
                                                                                                                                                                                                                                                                  Query Match
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DNM1_YEAST
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                               223 SESLKLAREVDPQGKRTIGVITKLD-LMDSGTNALD-ILSGKMYPLKLGFVGVVNRS--- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 QLAKQKAQEAEKLLNNVISKLLPTNTDIF------GLKISNSLILDVKAEPID 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 -----OTEQELARYGGVGATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 SESL-----LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD-LGVLQKSSAW 71
                   278 ---QQDJQ-----LNKTVEESLDKEEDYFRKHPVYRTISTKCGTRYLAKLL-----
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CY-1997 (Rel. 35, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-0ST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 9%; Score 97; DB 1; Length 757; Similarity 23.1%; Pred. No. 7.9; Conservative 35; Mismatches 74; Indels 22; Conservative 35; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H -> ISPD (IN REF. 1).
EBEF8793C5951770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 NESRASLV---LQLMNKFSTNFISSIDGTSSDINTKELCGGARIY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIF 223
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GTP (POTENTIAL).
GTP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, 273106; CAA974411; -. SGD: S0003924; DNM1.
InterPro: IPR001401; Dynamin.
InterPro: IPR00375; Dynamin_central.
InterPro: IPR003130; GED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00410; DYNAMIN; 1.
Hydrolase; Motor protein; GTP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L40588; AAA99998.1; -. EMBL; X91488; CAA62769.1; -.
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Pfam; PF01031; dynamin_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00195; DYNAMIN.
SMART; SM00053; DYNC; 1.
SMART; SM00302; GED; 1.
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SEQUENCE FROM N.A.
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Local Sim.
52;
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P53076;
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CONFLICT
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NCB1\_TaxID-4932;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 97; DB 1; Length 958; Best Local Similarity 22.7%; Pred. No. 11; Matches 58; Conservative 46; Mismatches 84; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 -IFGLKISNSLILDVKAEPIDDG-----KGLNLS----FPVTANVTVAGPIIGQIINL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 806 LYFELKLANYLVMIKKSSSKDDDEIENLILKGQELSNEFIYDTKIPQSLRDRFSGQLSNV 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           866 SALL ----- AYSNPLVEAPKEISGYLSDEYLQERLFQVSNNTILTFLHKDSECA---L 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 KASLDLLTAVTIETDPQTHQPVAVLGECASD-----PTSISLSLLDKHSQIINKFV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GVLTGTSESLLDNLGND---LSNVVDKL--EPVLHEGLETVDNTLKGILEKLKVDL---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 -----GVLQKSSAWQI.AKQK----AQEAEKLLN------NVISKLLPTNTD 98
                                                           Fartmann B., Kramer B., Kramer W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN 165 185 POLY-ASP.

DOMAIN 450 453 POLY-SER.

SEQUENCE 958 AA: 108178 MW; 335ADD152949F8C8 CRC64;
                                                                                                                                                                                                                                                                                                                                           SGD; S0003196; V1D30.
InterPoro; IPR003877; SPKY.
InterPoro; IPR003878; SPKY.
Pfam; PF'00622; SPRY; 1.
SMi.RT; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                       EMBL; 272749; CAA96943.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      916 ENVISNTRAMLSTELE 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
DOMAIN 165 18
                                            SEQUENCE FROM N.A.
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Search completed: August 6, 2002, 17:07:31

Job time: 873 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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OM protein - protein search, using sw model

August 6, 2002, 16:53:58 ; Search time 111.35 Seconds (without alignments) 386.850 Million cell updates/sec Run on:

US-10-020-139-2 Title: Perfect score: Sequence:

1 MLQLWKLVILCGVIJTGTSES..........NVIQQVVDNPQHKTQLGTLI 249

562222 seqs, 172994929 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_19:\* Database :

sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_fungi:\*
sp\_huma:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_organelle:\*
sp\_phage:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

## SUMMARIES

Description		Q9bqq0 homo sapien	Q96dr5 homo sapien	P79124 bos taurus	P79125 bos taurus	Q9d734 mus musculu	Q63471 rattus norv	Q63550 rattus norv	Q96hk6 homo sapien	Q61114 mus musculu	Q9d6p2 mus musculu	Q9d794 mus musculu	Q9cqx3 mus musculu	Q9d6p0 mus musculu	Q9d9j8 mus musculu	Q9bqp8 homo sapien	Q9smv6 arabidopsis
QI		09860	096DR5	P79124	P79125	090734	063471	063550	Q96HK6	061114	Q9D6P2	09D794	O9COX3	049G60	090938	Q9BQP8	90MS60
DB	; ;	4	4	9	9	11	11	11	4	11	11	11	11	11	11	4	10
% Query Match Length DB		249	249	243	240	235	235	206	484	474	235	270	270	270	232	199	1075
& Query Match		100.0	99.4	35.8	34.1	29.0	27.3	17.2	12.9	12.2	12.0	12.0	12.0	11.8	10.7	10.5	9.0
9	1	1233	1225	442	420.5	357.5	336.5	212.5	159	150.5	148.5	148.5	148.5	145.5	132	129	110.5
Result		-	7	М	4	ഹ	w	7	80	đ	10	11	12	13	14	15	16

	Q61769 mus musculu Q48995 mycoplasma Q9n218 caenorhabdi Q9ks47 vibrio chol Q9cka9 pasteurella Q9fvx8 oryza sativ Q99u54 staphylococ
099TN0 005701 099R31 099R31 098R31 098R31 097A36 095436 095436 099CEL 099CEL 099CP9 09	061769 Q48995 Q9N2L8 Q9K847 Q9CKA9 Q9FVX8
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	976 60 60 60 60 60 60 60 60 60 60 60 60 60
1187 1187 1188 1288 1288 1388 1388 1388 1388 1388	0644444 00012844

## ALIGNMENTS

8; Gaps

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Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/UDBJ databases.
EMBL; U79414; AAB38283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
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                                                                                                                                                                                                                                                                                                                                                                                 121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                            61 DIGVLQKSSAWQLAKQKAQEAEKILLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
BSP30, a bovine member of the Parotid Secretory Protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.1%; Score 420.5; DB 6; Length 240; 38.1%; Pred. No. 3.5e-23;
                                                                                                                  35.8%; Score 442; DB 6; Length 243; 38.9%; Pred. No. 9.5e-25; Live 58; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Indels
              Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79413; AAB38282.1: -.
SEQUENCE 243 AA; 26877 MW; 0C2D8DD45660E11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26513 MW; 850611DE9E43E358 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                96; Conservative
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"The cloning and sequencing of two cDNAs coding for alternate forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPINTDIFGLKISNSLILDVKAEPIDDG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ISLSLIDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verkatesh S.G., Geetha C., Gorr S.-U.; "A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DLGVLOKSSAWOLAKOKAQEAEKLINNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
        181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 99.6%; Pred. No. 7.8e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF432917; AaL28113.1; -. SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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19, Last annotation update)
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                                                                                                                                                                                                                                                                                         PAROTID SECRETORY FROTEIN.
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TISSUE-PAROTID GLAND;
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                                                                                          241 HKTQLQTLI 249
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EMBL; M83209; AAC06334.1;
                                                                                                                               Rattus norvegicus (Rat).
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Best Local S
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Q63550;
    063471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ra Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Anizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Osazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Rissi C., King B., Kochiwa H., Sakuli K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Schriml L., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Romstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anonso P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Salowa K., Schoenbach C., Seya T., Shibata Y., Sotoch K.-F., Wannia H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wannia K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wannia K., Wawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ښ</u>
170 ISLTVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDAECVEKLIGESO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DLGVLOKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSLILDVKAEPID 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 DKISISLIGRRLPIINSILDGVSTLLTSTVLQNFLCPLLQYVLSTLNPSVLQGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 DVELLQQATSWPLAKNSILET --- LNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKI,EPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AK009654; BAB26418.1;
MGD: MGI:97787; PSP.
SEQUENCE 235 AA; 27337 MW: AP90016602.235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.0%; Score 357.5; DB 11; Length 235;
                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AA.
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE=21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
                                                                                                                                                                                                                                                                                        PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                        241 HKTO 244
                                                                              230 DTTQ 233
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                                                                                                                                                                                                    090734;
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RESULT 6 Q63471 ID Q63471 063471

Matches

g ò qq ò Dp ò

RESULT 5
090734
10 090734,
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"Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG--LKISNSL1LDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 DVGSLOOATTWPSAKDSILET --- LNKV -- ELGNSNGFTPLNGLLLRVNKFRVLDLQAGL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 IDDGKGLNLSFPVTANVTVACPIIGQIINLKASLDLLTAVIIETDPQTHQPVAVLGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 DPTSISLSLADKHSQIINKFVNSVINTLKSTVSSLAQKEICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
NEONATAL SUBMANDIBULAR GLAND PROTEIN.
0B36EC779025986E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEOMATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
SMGB1/SMGB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirels L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland Bl-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Indels
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 336.5; DB 1 ilarity 31.8%; Pred. No. 4.5e-17; Conservative 62; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 267:2679-2687(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92129360; PubMed=1370829;
Mirels L., Ball W.D.;
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5

SEQUENCE FROM N.A.

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40; Gaps

21

CHAIN

Query Match

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proteins."

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118 DDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAV-LGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 TYNQELVVRIPLDMVAGLNTPLIKTIVEFQMSTEVQALIRVERSKS--GPAHLNLSDCSS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 LKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 LPL-LRAMODKSG-----SIPILDSFVHTVLKY---IIWMKVTSANILOLDVQPS 101
                                                                                                                                                                                                                                                                                                                                                                    173 ECASDPTSISLSLDRKHSQIINKFVNSVINTLKSTVSSLLQKEIGPLIRIFIHSLLVNVI 232
                                                                                                                                                                                                                                                                                                                                                                                                         33; Caps
                                                                                                                                                                                                                                             117 IDDGKGLNLSFPVTANVTVAG---PIIGQIINLKASLDLLTAVTIFTUPQTHOPV-AVIK 172
                                                                                                                                                                                                                                                                                                         102 SANDOELLUKIPLD----MVAGENTPLUKTIVEFHMTTE--AQATIRMDTSASGPTKLULS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snead M.L., Villanueva J., Paine M.L., Lei Y.P., Zhu D.H., Lusis J., Xia Y.-R., Yang J.-N.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U460668, PAMR7581.2:
Interpro: IPR001124: LBP_BPI_CETP.
SMART; SM00328: BPI1; 1.
SMART; SM00329: BPI2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WKLVLLCGVLTGT----SESLLDNLGNDLSNVVDKLEPVLHFGLETVDNTLKGLLEK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 WILTILGGLLGATIVQANVYPPAVI, NIGPEV ---- IQKHLTQALKDHDAT -- ATLQE 55
                                                                                                                          63 -----GVIQKSSAWQLAKQKAQEAEKLLNNVISKLI.PTNTDIFGI.KISNSI.II.DVKAEP 116
                                                                                                                                                              5 WKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKLKVDL 62
                                                        5 WIFTLECGLLAATE------IQATESPTAVEILG-------PKVIKEKLTUEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 NESTLRLSLLHKLSFVVNSLAKNVMNLLVPALPQIVKNHLCPMIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52373 MW; 377DBFA5E736709B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VON EDNER MINOR SALIVARY GLAND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
12.2%; Score 150.5; DB
Best Local Similarity 23.1%; Pred. No. 0.004;
Matches 52; Conservative 56; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D6P2
Q9D6P2;
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12.9%; Score 159; DB 4; Length 484; 23.9%; Pred. No. 0.00099;

Best Local Similarity

Query Match

Strausberg R.; Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2001); -. EMBL; BC008429; AAH08429.1; -. SEQUENCE 484 AA; 52427 MW: 08242B697284EB58 CRC64;

SEQUENCE FROM N.A. TISSUE-SKELETAL MUSCLE;

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Q96HK6; **096HK6** 

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RESULT Q96HK6

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                                                                                                                                                                                                                                                                                                                                                                                                     C STRAIN-C57BL/63; TISSUE-TONGUE:

RX MEDLINE-21085660; PubMed=11217851;

RATANAWA T. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa M., Nishi K., Konno H., Adachi J., Fukuda S.,

RA Alzawa M., Nishi K., Konoo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Shoon H., Kasikawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasikawa T., Saito R.,

RA Fielschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fielschmann W., Gasterland T., Oissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Late 409:85-690(2001).
EMBL: AK010143: BAB26728.1; -
MGD: MGI:1919687: 2310074819Rik.
AGD: MGI:235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
03-310021H06RIK PROTEIN.
        01-juN-2001 (TrEMBLrel. 17, Created)
01-juN-2001 (TrEMBLrel. 17, Last sequence update)
01-juN-2001 (TrEMBLrel. 17, Last annotation update)
2310074B19RIK PROTEIN.
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Matches 39; Conserv
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XX STARING-57BL/G51 TISSUE-TONGUE;

XX MEDLINE-21085660; PubMed-11217851;

X MAWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X MAWAI J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

X Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

X Alto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cachwa H.,

X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cachwa H.,

X Robin D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

X Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

X Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

X Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

X Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

X Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., A Radota K., Matsuda H.A., Gissi C., King B., Kochiwa H., A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., A Schrimi L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Rakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., A Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N. A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Whishaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A Whishi Yaki V.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310021H06RIX PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK009441; BAB26290.1; -.
MGD; MGI:1914385; 2310021H06Rik.
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les 39; Conservative
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STRAIN-CSTBL/61; TISSUE-TONGUE;

K Kawai J. Shinagawa A., Shibuta K., Konno H., Adachi J., Fukuda S., Arakawa T., Shinagawa A., Shibuta K., Konno H., Adachi J., Fukuda S., A Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raito T., Okazaki Y., Golobori T., Bono H., Kasikawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Rohrigh L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownsteln M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., Asasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Sakaudi H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mushawachiyaki S., Hawseqawa Y., Kawaji H., Kohtsuki S.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 INEKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLON-LIDSLTDI 224
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 148.5; DB 11; Length 25.3%; Pred. No. 0.0028; tive 38; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492A16EEBAB4A677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1914386; 231002±H06Rik.
SEQUENCE 270 AA.
                                                                                                                                                                                EMBL, AK010115; BAB26710.1; --
EMBL, AK009329; BAB26221.1; --
EMBL, AK009531; BAB26343.1; --
                                                                                                                                                                                                                                                                                                                                  AK009580; BAB26372.1; -. AK009629; BAB26401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK010012; HAB26642.1; -. AK010051; BAB26667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           AK009695; BAB26444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AK009803; BAB26513.1; -. AK009835; BAB26533.1; -.
                                                                                                                                                                                                                                                                                                AK009562; BAB26360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                     Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2310021H06RIK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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K Kawai J., Shinagawa A., Shibata K., Koohino M., Itoh M., Ishii Y.,

K Kawai J., Shinagawa A., Shibata K., Koohino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Koono H., Adachi J., Fukuda S.,

A Azawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rakull L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakull L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakuki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Rakuki M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rakuki M., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

Rayuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rayanawa Bois A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Rayanawa Mynshwa-Bois A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                              84 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGOI 143
                                                                                                                                                                                                                                                                  108 VLGKVISS-IPLI,NNILDIRVINPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSI, 166
                                                                                                                                                                                                                                                                                                                            144 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                       4 LWK-LVLLCGVLT-----GTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTL 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Kukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                      DB 11; Length 270;
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                                                                                                                                   , Match
Local Similarity 25.3%; Pred. No. 0.0046;
Les 39; Conservative 38; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA; 25713 MW; 0D52D24A3076D5DC CRC64;
Nature 409:665-690(2001).
EMBL: AK010145; BAB26730.1J. -.
MGD; MGI:1914385; 2310021406R1k.
SEQUENCE 270 AA; 29235 MW; A86F02ABBAAFBCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              204 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 LTRVIPGLVOGVVCPLVNGVLSLLDVTLAHDVAD 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700058C13RIK PROTEIN.
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Best Local Similarity
Thes 55; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_TaxID=10090;
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106 NSLILDVKAEPIDDGKGLNLSFP---VTANVTVAG------PIIGQIINLKASLDLLTAV 156
                                                                                         102 ------DCGGIQMAFPKEWFSANITLEFDIEFKLPFNSNIIKTHACMGLTAES 148
                                                                                                                                       157 TIETDPQTHQPVAVIGECASDPTSISLSL-LDKHSQIINKFVNSVINTLKSTVSSLLQKE 215
                                                                                                                                                            149 WLEKDEFGRREL-VMGRCRMEPSSGGASMSTEETSPKMKHFLHNLRESLGKVIPNLVESQ 207
52 KG-----ILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 105
                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49G10.6 (SIMILAR TO MURINE VON EBNER MINOR SALIVARY GLAND PROTEIN, ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracey A.; submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. submitted (JUN-2001); CAC03550.1; -. NON_TER 1199 199 AA; 21517 MW; 49A4CC2143BE04BI CRC64;
                                                                                                                                                                                                                                                                                                                                          199 AA.
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                 216 ICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                     208 VCPLIGEILRQLDVKLLKGLV 228
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                         RESULT 15
Q9BQP8
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Search completed: August 6, 2002, 17:09:28 Job time: 930 sec

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(without alignments)
199.620 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQLWKLVLLCGVLTGTSES.....NVIQQVVDNPQHKTQLQTLI 249
                                                                                                                                                                                                                                                                         August 6, 2002, 16:47:18 ; Search time 138.55 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           OM protein . protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Human parotid secr	numan parotid secr	numan PROIDES prot	Human secreted pro	Human secreted pro	numen process sedu	Peptide #8941 enco	Human brain expres	Human bone marrow	Peptide #9264 enco Mouse 28.6 kDa sec	***
SUMMARIES	ID	AAW69221	AAW60682	AAB24069	AAB25765	AAB75351	AAM25745	ABB41435	AAM62308	AAM75111	AAM35227	AAE05367	
	DB	19	19	21	21	22	22	22	22	22	22	22	
	Length	249	249	249	249	249	260	50	20	50	50	278	
dЮ	Query Match Length DB ID	100.0	100.0	100.0	100.0	100.0	6.96	20.0	20.0	20.0	20.0	15.5	
	Score	1233	1233	1233	1233	1233	1195	246	246	246	246	191.5	
į	No.	н	2	c	4	Ŋ	9	7	80	ወ	10	11	

Human secreted pro LS170 polypeptide Amino acid sequenc Human secreted pro Human PRO polypept Human polypeptide	tuman bon Human dig Human dig Human NoV Human NoV Human NoV Walno acol Luman PRO Human PRO Human PRO Human PRO Human PRO Human PRO Human PRO Human Seci Human S	Recombinant endoto Amino acid sequenc Human KSP. Homo s Haemophilus influe Human secreted pro
AAY064 AAW954 AAY691 AAU390 AAU292 AAM3972	22 AAM92209 22 AAM92212 22 AAM92213 22 AAM92214 22 AAM92214 22 AAM97214 22 AAM97216 22 AAM77206 22 AAM66124 22 AAM66124 22 AAM66124 22 AAM66124 21 AAW88397 22 AAM97370 22 AAM977018	AAG6741 AAB4721 AAU3558 AAY0269
9999999	2664 1907 1917 1917 1918 1918 1918 1918 1918 191	1220
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183.5 183.5 183.5 183.5 183.5	193.5 9.3.5 16.5 16.7	100 100 99 98.5
12 13 14 15 17 18	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 2 8 4 4 8

## ALIGNMENTS

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Parotid secretory protein; hpsp. digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                                                                                       /note= "signal peptide"
                                                                                                                                                                 19..249
/note= "mature hPSP"
                AAW69221 standard; Protein; 249 AA.
                                                                                                                                         Location/Qualifiers
                                                                   Human parotid secretory protein.
                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                              97WO-US23522.
                                                                                                                                                                                                                                               96US-0034429.
                                                16-OCT-1998 (first entry)
                                                                                                      therapy: diagnosis,
                                                                                                                                                                                                                                                                                Duan R, Ruben SM;
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                             23-DEC-1996;
                                                                                                                                                                                          WO9828420-A1
                                                                                                                                                                                                                            18-DEC-1997;
                                                                                                                                                                                                            02-JUL-1998
                                  AAW69221;
                                                                                                                                                Peptide
                                                                                                                                                                 Protein
        AAW69221
RESULT
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Interaction. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting).

Consider the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting).

Consider the corresponding genomic DNA. The DNA and protein can be maplification or immuno assays), particularly for diagnosis of diagnosis of cancers of the saltwary gland, thymus and application is diagnosis of cancers of the saltwary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibocerial, antiporasitic and antiviral agencia and may be expressed in vivo from the DNA. The protein, or cells carbagonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids which are potentially useful for treating conditions associated to the express the recombinant protein and this can be used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal tissue; HSPSP, Sjorgen's syndrome; Graves disease; thyroidlis; insulin-dependent diseets; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the human parotid secretory protein (hPSP) of the
                                                          New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1233; DB 19; Length 249; 100.0%; Pred. No. 1.2e-100; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW60682 standard; Protein; 249 AA.
                                                                                                                                             Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hPSP-binding proteins.
WPI; 1998-377651/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 AA;
                      N-PSDB; AAV44759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW60682
qq
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This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to granteet cancer and autolimume diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNV1QQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKG1LEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1233; DB 19; Length 249; 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-C; 65pp; English.
                                                      97WO-US20651.
                                                                                              96115-0749288.
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                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 249; Conservative
                                                                                                                                                                                                                                                                                                             gastrointestinal tissues
                                                                                                                                                                       Bandman O, Goli SK;
                                                                                                                                                                                                          WPI; 1998-297933/26.
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                                                                                                                                                                                                                                 N-PSDB; AAV37699.
                                                      07-NOV-1997;
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                22-MAY-1998
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PRO genes. Exemplary conditions or disorders to be treated with supplicing antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalanic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC5816 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC5836 to AAC5836 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO390, PRO311, PRO535, PRO619, PRO717, PRO809, PRO8103, PRO9183, PRO91025, PRO1030, PRO1093, PRO9107, PRO1111, PRO1133, PRO1109, PRO1083, PRO9105, PRO1184, PRO2145, PRO1184, PRO5145, PRO5145, PRO5161, PRO513, PRO31710, PRO2094, PRO3145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell growth. The PRO polypoptides and nucleotides are useful in the treatment, disagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to creat various conditions, including those characterised by overexpression and/or activation of the amplified
                                                  Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; neotropic; neuroprotective; antiinflammatory; immunosupressive; immunostimulant: antianglogenic; leukaemia; lymphoid malignancy; neuronal disorder; glaid disorder; astrocytal disorder; angiogenic; hypothalantc disorder; glandular disorder; macrophagal disorder; inflammatory disorder; immunologic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis and prevention of cancer
                 Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US12252.
99US-0141037.
99US-0143048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                            14-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment,
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ROY MA;

septic shock; impotence.

Homo sapiens.

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This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAARY125-AB774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequence data on a computer system, and a methods for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L., Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                            98us-0113686.
99us-0141032.
                                                                                                                                                                                                                                                                                99WO-1B02058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA87727
                                                                                                                                                                                                                     WO200037491-A2
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Gaps

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Indels

100.0%; Score 1233; DB 21; Length 249; 100.0%; Pred. No. 1.2e-100;

100.0%; Prec. ....

Best Local Similarity 100. Matches 249; Conservative

Query Match

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Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardlovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondricoytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                           121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                   181 ISLSELDKHSOIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                           61 DLGVLOKSSAWQLAKOKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                             1 MLQLWKI.VLI.CGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKG1LEKLKV 60
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Query Match
Best Local Similarity
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                                                            249 AA;
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                                                               Seguence
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proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                   121 KGLNLSFPVTANVTVAGPLIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                       181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                         61 DLGVLOKSSAWOLAKOKAOFAEKLLNNVISKLLPTNTDIFGLKISNSL1LDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                               121 kglnlsfpvtanvtvagpilggiinlkasldlltavtietdpgthgpvavlgecasdpts 180
                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                       1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
                                                                                                                                                          100.0%; Score 1233; DB 21; Length 249; 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bougueleret L, Jobert S;
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                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75351 standard; protein; 249 AA.
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99US-0469099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2001 (first entry)
                                                                                                                                                                                   249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-071487/08.
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                               241 hktqlqtli 249
                                                                                                                       249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1999;
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                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75351;
                                                                                                                                                             Query Match
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immunostimulant, gene therapy, antisense therapy; vaccine; inflammation, antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia, antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ISLSI.LDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ULGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIQIMKLVLLCGVLTGTSESLLINLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
The present invention relates to 49 Secreted proteins and the CDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
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                                                                                                                                                                                                                                                                                               100.0%; Score 1233; DB 22; Length 249; 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                                                         Indels
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O
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                               100.00;
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000WO-US35017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder.
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AAM62308
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    AAM2563. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinifammatory; antinheumatic; cells they are expressed in, such as: antinifammatory; antinheumatic; cardiantstructs; immunosuppressive; antibacterial; endocrine; cardiant; cardianeamic; antibacterial; endocrine; cardiant; cardianeamic; antibacterial; endocrine; cardiant; cardianeamic; antibacterial; antimaterial; antibacterial; outperformatic) antidabetic; oytostatic; neuroprotective; antidapressant; nootropic; antidaprexisonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antigonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunocytices, neurodegenerative and incombined inclusions, adderess, parkinson's disease, neurodegenerative and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 dlgvlqkssawqlakqkaqeaekllnnviskllptntdifglkisnslildvkaepiddg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHOPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 islelldkhsqiinkfvnsvintlkstvssllqkejcplirifihsldvnviqqvvdnpq 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLQLWKIVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 mlglwkivllcgvltgtseslidnigndisnvvdklepvlhegletvdntlkgileklkv 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.9%; Score 1195; DB 22; Length 260; Best Local Similarity 97.2%; Pred. No. 2.7e-97; Matches 242; Conservative 1; Mismatches 6; Indels 0;
                                                                                                                         Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB41435 standard; Peptide; 50 AA.
Tany YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorders.
                                WPI; 2001-457603/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 AA;
                                                 N-PSDB; AAH99686
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Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.2e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 piiggiinlkasldlltavtietdpgthqpvavlgecasdptsislslld 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                               2000US -0180312.
                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000US-0608408
                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-0024263
                                                                                                                                       30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483447/52.
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WO200157277-A2
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                                                                                                                                                                                                               04-FEB-2000;
                                                                       09-AUG-2001
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us-10-020-139-2.rag

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leuksemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #9264 encoded by probe for measuring placental gene expression.
                                             The present invention provides a number of single exon nucleic acid
                Example 4; SEQ 1D NO: 35417; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                       20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                     138 PIIGOIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                      1 piiggiinlkas1dlltavtietdpgthgpvav1gecasdptsis1s11d 50
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta -
                                                                                                                                                                                                                 100.0%; Pred. no.
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                                                                                                                                                                                                                                                                                                                                                                                   AA.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
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2000US-0236359
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04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2001 (first entry)
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                           50 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 AAM35227;
                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schlzophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ 1D NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
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                                                                                                                                                                                                                      Example 4; SEQ 1D NO: 34413; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                            Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM75111 standard; Protein; 50
                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0207456.
2000US-0608408.
                            27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-0024263.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM75111:
                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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20.0%; Score 246; DB 22; Length 50;
Query Match
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6

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The proteins which play a major role in induction of growth, cell migration and proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise anticonedies, to guantitatively determine bevels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or states. Compositions comprising the novel proteins of the invention are useful in genome and physical mapping, in positional cloning of are useful in genome and physical mapping, in positional cloning of genes, to tag or indentify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as immunoregulatory and anti-inflammatory molecule, as anti-cancer treatment, and as a starget for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant.

The present sequence is 28.6 kba protein, a secreted protein from mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, cytostatic; antlinflammatory; immunoregulatory; tissue integrity; wound healing; immune response; vaccine; cancer; asthma; allergy; cell trafficking; therapy; 28.6 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses novel polynucleotides and their corresponding
                                         .;
0
                                                                                138 PIIGQIINLKASLDLLTAVTIETDIVQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                       Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                     AAE05367 standard; Protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 92; 101pp; English.
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                Mouse 28.6 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2000; 2000US-0724864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0171678
                                                                                                                                                                                                                                                                                                                       12-SEP-2001 (first entry)
                  Lecal Similarity 100.
nes 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson JD, Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-425665/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD10135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO200148192-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2001.
                                         Matches
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278 AA;

Sequence

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61 spalpsnptdllagkftdalsgql-----lsggl-----1gileniplldviksgggn 108
                                                                                                                                                                                         81 AEKLLNNVISKL---LPTNTD[FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG 137
                                                                                                                                                                                                         138 PIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLLDKHSQIINK 195
                                                                                                                                                                                                                                                                                169 pvvgsllglavklnitaevlavkdnggrih---lvlgdcthspgslkisllngvtp-vgs 224
                                                                                               l mflvgslvvlcgllahstaqlaqlplplgqgpplplnqgpplplnqgqllplaqglplav 60
                                                                                                                              30 ----SNVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel human secreted protein, termed nh796_1. The sequence is predicted from a full-length cDNA clone (see AAX59356) isolated from a human adult brain (thalamus) cDNA library. The invention provides cDNA clones (see AAX59352-58)
                                   61;
        DB 22; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; nh796_1; human; brain; thalamus; therapy;
                                                                                                                                                                                                                                                                                                                               225 fldnltgiltkvlpeliggkvcplvngilsgldvtlvhniaellihglq 273
                                                                                                                                                                                                                                                                                                               196 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
    15.5%; Score 191.5; DB 22; Length 23.2%; Pred. No. 7.4e-09; Live 50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "predicted leader/signal sequence" 20..256
                                                                  1 MLQLWKLVLIGGVLTGTSESLLD------NLGNDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs K, LaVallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg D, Steininger RJ, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06408 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0222653.
98US-0070346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US27903
Ouery Match
Best Local Similarity 23.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-419350/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX59356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9935252-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aqostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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78 kpgggtsggilggilgkvtsvipglnniidikvtdpglleiglvgspdgnrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                  132 NVTVAGPLIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 klqvntplvgasilrlavklditaeilavrdkqerihl-vigdcthspysiqisildglg 196
encoding novel secreted proteins (see AAY06404-10) of the human tests, brain and foetal kidney. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell provided. Suggested activities include nutritional, cytokine, cell vaccine) or immunosuppressive, haematopoiesis regulating, tissue affectivit or inhibin; chemotactic or chemokinetic, haemostatic, thrombolytic, receptor/ligand, antiinflammatory, cadherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                        Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                       75 KOKAQEAEKLLNNVISK---ILPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                            15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLGVLGKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                         45 tglagsitnaisngl.....lsggl.....lsggl......igilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 183.5; DB 20; Length 256; 23.8%; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New 5.5170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;
Roberts-rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Friedman PN;
                                                                                                                                                                                                                                                                                      Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colpitts TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                     46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen M,
                                                                                                                                                                                                                                                              Best Local Similarity 23.89
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSi70 polypeptide sequence
                                                                                                                                                                                                         256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-060335/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Billing-medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX00809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9856951-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1998;
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                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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    8x366666666666688
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                                                                                                                                                                                                                                                                                                                                       qq
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Sequences AAM95463-47) represent LS170 polypeptide fragments which contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polynucleotide that comprises treating a test sample with at least one LS170 specific nucleic acid that with any of the sequences (AAX080109) are fragments derived from various clones of LS170 gene. The LS170 overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment such disease. Particularly detection of LS170 polynucleotide, IS170 or ling disease. Particularly detection of LS170 polynucleotide, IS170 cantigens, or anti-LS170 antibodies is indicative of disease. Cells sequences are used to expression system comprising the LS170 nucleic acid care used to expression system comprising the LS170 nucleic acid sequences are used to express recombinant polypeptides. The polypeptides can be used to express recombinant polypeptides. The polypeptides can be used to isolate related sequences; as standards and reagents in therapeutic agents (by neutralising LS170 related nucleic acid assays; as targets for drug screening, and as components or targets for used to deliver therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 KQKAQEAEKILUNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 kpggqtsggliggligkvtsvipglnnlidikvtdpqlleiglvqspdghrlyvliplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 NVTVAGPIIG-QIINLKASLDI.LTAYTIETDPOTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 kigyntplygasiirlavkiditaeilavrdkgerihi-vigdcthspgsigislidgig 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 tglagsitnalsngl-----lsygl-----lgilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIF1HSLDVNVIQOVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 183.5; DB 20; Length 256; 23.8%; Pred. No. 3.4e-08; tive 46; Mismatches 100; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun Y, Recipon H, Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY69164 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0095233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200008206-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang F,
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Lung specific genes for developing products for diaynosing, monitoring, staging, prognosticating, imaging and treating lung cancer
                                                                                                                                                                                                 The present sequence is encoded by a lung specific gene, designated Lug110, clone ID 1355520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer. Sepecially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for
                                                                                                                                                          Example 2; Page 35-36; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               treating lung cancer.
                      WPI; 2000-195589/17.
                                            N-PSDB; AAZ61165
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                                                                                                                                                             75 KQKAQEAEKLLNNVISK----LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                      46; Mismatches 100; Indels 33; Gaps
                                                                                                                      45 tglagsltnalsngl-----lsggl----lsggl----lgilenlplldil 77
                                                                             15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
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Human; secreted protein; antiinflammatory; immunosuppressive; nouroprotective; antiarthritic; antimicrobial; vulnerary; overstric; antidatetic; virude; antiinfertility; antidonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; ererbroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; altonor; periodontal disease; osteoporosis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; stroke, sepsis; inflammatory bowel disease; contraceptive; immunogen; stroke, sepsis; inflammatory bowel disease; contraceptive; immunogen; AAU39019 standard; Protein; 256 AA. Human secreted protein nh796\_1. 16-JAN-2002 (first entry) food supplement; vaccine. AAU39019

AAU39019

XXX
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AAU3

XXX
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B Human

XXX
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; 6

WO200175068-A2. Homo sapiens. 11-OCT-2001.

Search completed: August 6, 2002, 16:52:51 Job time: 333 sec

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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation acilvity or may induce production of other or cell differentiation acilvity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune auticiacides and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rhemmatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and uncers; as well as in treatment of periodontal disease, diseases of the peripheral nervous system, amploing lateral sclerosis or osteoarthritis, mediated by infanction of cardiac and central nervous system vessel e.g. stroke, amplotrophic lateral sclerosis, and Shy-Darger syndrome, infections, infanction of cardiac and central nervous system vessel e.g. stroke, sepsis, infiammatory bowel disease, uncers, bone regeneration. The protein, having activin- or inhibin-relaced activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The
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                                                                                                                                                                                                                                                                                                                                                                   Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
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J, Steininger RJ, Spaulding V, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 497-498; 619pp; English.
                                                                                                                                                                                                                                             Merberg D;
                                                                                              04-DEC-2000; 2000US-0729674.
                                                                    30-MAR-2000; 2000US-0539330.
                     22-MAK-2001; 2001WO-US09369
                                                                                                                                           (GEMY ) GENETICS INST INC.
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Treacy M, Agostino MJ,
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Page 10

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 358.294 Million cell updates/sec August 6, 2002, 17:05:10 ; Search time 66.51 Seconds Run on:

US-10-020-139-2\_COPY\_2\_249

1 LQLWKLVLLCGVLTGTSESL.......NVIQQVVDNPQHKTQLQTL1 248 Title: Perfect score: Sequence:

Scoring table:

Gapup 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* 4: pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

micross-references: GB:M26807; NID:9200556; PIDN:AAA40009.1; PID:9554264 C;Comment: PSP is the most abundant protein in the parotid gland. Its function is no C;Genetics:

A.Gene: Psp.
A.Map position: 2
A.Nutrons: 14 1/1
A.Nutrons: 14 1/2
A.Nutrons: 15 4 0/1
A.Nutrons: 15 4 1/2
C.Kcywords: parotid gland; saliva
F:1-20/Domain: signal sequence #status predicted <AIS>
F:21-235/Product: parotid secretory protein #status predicted <AAI>

2.QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61

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qq ò

Query Match 29.3%; Score 359.5; DB 1; Length 235; Best Local Similarity 33.6%; Pred. No. 4.2e-19; Matches 80; Conservative 62; Mismatches 79; Indels 17; Gaps

Query Match

R 0 0 1 1 1 1		% € 0.00			SUMMARIES	
NO.	Score	Match	Length	DB	QI	Description
٦	59	6	235	7	SOMS	parotid secretory
7	31		235	~	B42337	V)
٣	207.5	16.9	206	~	A42337	
4	10		1075	~	T52638	
S	10		1075	7	T51557	1 (XPO1)
9	109		1769	2	.553378	membrane
7	108		825	~	8994	hypothetical prote
ω	106		296	7	A49943	fructose-bisphosph
6	104.5		473	7	S17448	probable ligand-bi
10	104.5		72	7	T50073	myosin-like coiled
11	104	•	1616	7	G64242	cytadherence-acces
12	104		71	N	A37052	
13	103.5	•	29	7	F90067	
14	100.5	•	1056	П	G02157	in-like
. 15	100		99	7	C82759	
16	99.5		1524	7	868553	surface layer prot
17	66		619	7	D64182	DNA ligase (NAD+)
18	66		1441	7	B86807	ဥ
19	98.5		61	_	WMTM8T	180K protein - tom
20	86		521	~	534338	biliary qlycoprote
21	97.5		211	~	D64505	hypothetical prote
22	97.5		414	7	T27045	hypothetical prote
23	97		757	Н	S64742	
24	97		958	~	S64249	hypothetical prote
52	96.5		328	~	A82087	
56	96.5		1345	ď	H90975	
27	96.5		99	~	E85822	asin
28	96		458	7	JC1509	qlycc
29	96		624	~1	PC6003	rface membrane

		30	96	7.8	1005		A64465	hypothetical prote
		31 95	5.5	7.8	2938	2	T30249	cell proliferation
		32	95	7.7	256		877810	probable DNA topoi
		33	95	7.7	578	7	н 82204	methyl-accepting c
		34	95	7.7	1130		T19148	hypothetical prote
		35	95	7.7	6713		B89921	hypothetical prote
		9	5.5	7.7	292		H89824	conserved hypothet
		7	94.5	7.7	1729		557596	ribosomal RNA proc
		8	94	7.7	462		T10094	nitrogenase (EC 1.
/sec		39	94	7.7	490		D84999	ketol-acid reducto
			3.5	7.6	640		T03754	hypothetical prote
			10.	7.6	722		H97217	uncharacterized on
			. 2	7.6	868	0	S65186	NIP80 protein - ve
	_		5.5	7.6	1038		537854	ř
			63	7.6	206		A40305	biliary glycoprote
		45	603	7.6	752	2	T09649	delta-1-pyrroline-
							ALIGNMENTS	
	RESULT	LT 1						
	SQMS	SQMS parotid secretory protein precursor	retory	prote	in prec	curse	or - mouse	
	N;Al	N; Alternate names: PSP	names:	PSP				
	C; Sp	C. Species: Mus musculus (house mouse)	Aus mus	culus	(house	IOII e		
	C; Po	C.bace: 31-Dec-1988 #sequence_revision C.Accession: A23031: I53236	Jec-198 : A2303	1: I5	Juence_ 3236	-rev	31-Dec-1988	<pre>#text_change 22-Jun-1999</pre>
	R; Ma	R; Madsen, H.O.: Hinth, J.P.	C	orth,	J.P.			
			1		13, 1-13, 1985	1985		
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	re de la company	}	2	GB:	GB:X01697;	IN	NID:953810; PIDN:CAA	NID:953810; PIDN:CAA25846.1; PID:9758163
				, 1986	, p.v.;			b.m.; haimark, K.; Nielsen, J.I.; Hjoren,
.*	1500 ·	2	<u> </u>	1.01 (53)	f murin	ne pë JID:{	h of murine parotid secretory protein and 153236; MUID:87004556	rotein and salivary amylase expre
-	>		Ř.		ransla	ted	translated from GB/EMBL/DDBJ	
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r.		C.Comment. DSD is the most abundant	20 1a	, pa 4	ide to		it protein in the	is the perceid also disperior is a

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A; Description: functions as nuclear export receptor for proteins carrying leucine-ric C; Superfamily: Arabidopsis thaliana exportin 1
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Plant J. 201, 695-705, 1999
A.F.Itle: Nuclear export of proteins in plants: AtXPOl is the export receptor for leuch A;Reference number: 226149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                          58 KVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID 117
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712 QISLIFLDM------LNVYRMYSELVSTNITEGGPYASKTSFVKLLRSVKRETLKL 761
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      3 QLGSLVVLCGLLIGTSGSLFDIFQNPELDVESVWSEINYRIRYALETMDLDMLADYLSKR 62
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-1075 - HAAA
A;Cross-references: EMBL:Y18469; PIDN:CABB9280.1
A;Experimental source: cultivar Columbia; 3wk-old green vegetative Lissue C;Genetics:
                                                                                                                                                           5 KIVILCG----VLTGTSESILDNLGNDLSNVVDKLEP-VLHEGLETVDNTLKGILEKLK 58
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Best Local Similarity 23.8%; Pred. No. 4.5;
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J. Biol. Chem. 267, 259-2587, 1992
A;Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein ar
A;Reference number: A42337; MUID:92129360
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J. Biol. Chem. 267, 2679-2687, 1992
A:Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein an
A:Reference number: A42337; MUID:92129360
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                                                                                                                                                                                                                                                                    C;Species: Rattus norveyicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Aug-1999
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C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
C.Accession: A42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 DKISISLIGRREPFVNRILDGVSGLLTGAVSILLQNILCPVLQYLLSTMSGSAIQGHISN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 DCKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GVLQKSSAWQLAKQKAQEAEKLLNNVISKLI,PTN--TDIFG--LKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QLGSLVVLCGLI,IGTSESLLGDVANAVNN------LDILLNSPSEAVAQNLNLDV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QLWKLVLLCGVLTGTSESLLDNLGN...DLSNVVDKLEPVLHEGLETVD.NTLKGILEKL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:MB3210; NID:g206989; PIDN:AAC12783.1; PID:g206990 A;Note: sequence extracted from NCBI backbone (NCBIN:78707, NCBIP:78708) C;Superfamily: parotid secretory protein
                             180 ISLSLLDKHSQ11NKFVNSV1NTLKSTVSSLLQKEJCPLIR1F1HSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M83209; NID:g206456; PIDN:AAC06334.1; PID:g206457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: sequence extracted from NCBI backbone (NCBIN: 78709, NCBIP: 78710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.0%; Score 331.5; DB 2
31.7%; Pred. No. 4.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Mismatches
                                                                                                                                                                                                               parotid secretory protein precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: Psp
C,Superfamlly: parotid secretory protein
C,Keywords: parotid gland; saliva
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Les 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-235 <MIK>
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                                                                                                                                                                                                                                          N, Alternate names: PSP
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A,Cross-references: EMBL:X85021; NID:9728698; PIDN:CAA59385.1; PID:9728701
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, February 19º
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SA1447 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 SILTFLDKEDKPVCDKFITSYTKSIAKYDRS-----KLNIILSLLKK-----IRLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 EVKLIITDLIYLSEILEDKSQLVELFEYFISINEDLVLKCL------KSLGLT----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 VTVAGPIIGQIINLKASLDLLTAVTIETD - PQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 -----GELFEIRLTTSLFTNADVNTDIVKQLSDPV----ETTKKDTASFQTFLDKHS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.55;

Best Local Similarity 24.78; Pred. No. 4.8;

Matches 72; Conservative 39; Mismatches 94; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 TKEAIISYLSSDLFKGVGKKTAQNIVNTLG-------DNAINDILD----DHSVLEK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 SSAWQLAKQKAQEAEKL-LNNVISKLLPTNTDI-FGLKISNS-------106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 VSGLSKKKQK-QIAEQISANQESEKIMIRLHDLGFGPKLSMAIYQFYLGDTLTILDRNPY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 -LILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD----P 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 QLIYDIK-----GIGFNKADQLARNIGIA---YNDNERLKAAL----LYTLEEECIKQG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 EAEKILLNUVI--SKILLPTNTDI-----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 131
                                                                                                                                                                                                                                                                                                                                48; Mismatches 93; Indels 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  19 SLLONLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 78
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                                                                                                                                                                                                                                       Score 109; DB 2; Length 1769; Best Local Similarity 19.2%; Pred. No. 11; Matches 52; Conservative 48; Mismatches 93: 1727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 AAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                            C: Keywords: transmembrane protein
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             A; Residues: 1-1769 <RAF'>
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A; Introns: 33/3; 72/3; 103/3; 127/3; 163/3; 191/2; 237/3; 260/3; 286/3; 307/3; 322/3; 35
A; Introns: 33/4; 1000/3; 1035/3
A; Note: F2K13 170
C; Superfamily: Arabidopsis thaliana exportin 1
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Probable membrane protein VJJJ09c · yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J0808
N:Alternate names: hypothetical protein J0808
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
R;Rasmussen, S.W.
submitted to the EMBL Data Library, February 1995
A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and
A;Reference number: S53376
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #Lext_change 16-Feb-2001 C;Accession: T51557 F;Sato, S; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000 A;Reference number: 225394 A;Accession: T51557
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Yeast 11, 873-883, 1995
A;Title: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3
A;Reference number: S57357; MUID:96090136
A;Recession: S57359
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VDLGVLQKSSA----W-QLAKQKAQEAEKLLNNVISK----LLPTNTD-----IFGLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ISNSLILDVKAEPIDDGKGLNL----SFPVTANVTVAGPIIGQ--IINLKASLDLLTAVT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 IET--DPQTHQP-----VAVLGECASD-PTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 RD-EYLQRLMALPNQKWAEIIGQARHSVEFLKDQVVIRTVLNILQTNTSAATSLGTYFLS 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Mismatches 107; Indels 65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KLVLLCG-----VLTGTSESLLDNLGNDLSNVVDKLEP-VLHEGLETVUNTLKGILEKLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1769 <RAW>
A;Cross-references: EMBL:249384; NID:91008292; PID:91008293; MIPS:YJL109c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.0%; Score 110.5; DB 2; Length 1075;
Best Local Similarity 23.8%; Pred. No. 4.5;
Matches 68; Conservative 46; Mismatches 107; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    822 VPHIFEAVFQ---CTLEMI-----TKNFEDYPEHRLKFFSLL 855
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                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1075 <SAT>
A;Cross-references: EMBL:AL391141
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A; Molecule type: DNA
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Db 241 HTYLPINVVIDLTVDVLNYQDEEVIEPEKLUEMLQYLNEEKRLIIDNEQVAIPSLYYSE1 300	Db 68 GGLLGGGGLLSYGGLFSLVEELSGLKIEELTLPTVSIK 105
Qy 216 CPLIRIFIHSLDVNVJQQVVDNPQHKTQLQTL1 248	Qy 113 AEPIDDGKGINLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVIGE 172   1   1   1   1   1   1   1   1   1
A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - Staphylococcus carnosus (strain TM300) C;Species: Staphylococcus carnosus (crate: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 15-Oct-1999 C;Accession: A49943; S33358 R;Witke, C.; Goetz, F.	QY         173 CASDPTSISI.S*
J. Bacteriol. 175, 7495-7499, 1993 J. Bacteriol. 175, 7495-7499, 1993 A. Fille: Clohing, sequencing, and characterization of the gene encoding the class I fruct A. Reference number: A44943. MUID: 94042330 A. Status: A49943 A. Status: preliminary A. Molecule type: DNA A. Residues: 1-296 <wht> A. Residues: 1-296 <wht> A. Cross-references: EMBL:X71729; NID:q297873; PIDN:CAA50663.1; PID:q297874 C. Keywords: aldehyde-lyase; carbon-carbon lyase</wht></wht>	RESULT 10 T50073 myosin-like coiled-coil protein sp8 [imported] · fission yeast (Schizosaccharomyces F 7: Species: Schizosaccharomyces pombe C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 C; Accession: T50073 R; McDougall, R.C.: Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. Submitted to the EMBL Data Library, December 1999
Ouery Match  8 68; Score 106; DB 2; Leng Best Local Similarity 25.9%; Pred. No. 1.7;  Matches 50; Conservative 31; Mismatches 64; In  51 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTD  1 H: HIH  : :::	A; Nexestion: T50073 A; Accession: T50073 A; Status: preliminary: translated from GB/EMBL/DDBJ A; Status: preliminary: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1727 - CMCD> A; Cross-references: EMBL:ALl33357; PIDN:CAB62414.1; GSPDB:GN00066; SPDB:SPAC1486.04c A; Experimental source: strain 972h(-); cosmid c1486 C; Genetics: A; Gene: SPDB:SPAC1486.04c A; Map position: 1
ON 119 VAREITUDINGLANDS FYTAND TANGET IN THE STANDARD STA	Query Match Best Local Similarity 24.3%; Pred. No. 23; Matches Sj. Conservative 41; Mismatches 94; Indels 61; Gaps 11; Oy 17 SESLLDNIGNILARDIAL FOR THE STATE STAT
Db 261 SRALVSDLNAQOS 273 RESULT 9 \$17448 probable ligand-binding protein RYA3 - rat C:Species: Rattus norvedicus (Norway rat)	CY 49TLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLEPTNTDIF 99  1 :
	Qy 159 TDP/QTHQPVAVIACECASDPTS1.SL.LDKHSOLINKFVNSV1NTLKSTVSSLLQKEICPL, 218
A; Residues: 1-473 < DEA> A; Residues: 1-473 < DEA> A; Cross-references: EMBL:X60658; NID:957733: PIDN:CAA43065.1; PID:957734  Query Match Query Match Best Local Similarity 21.0%; Pred. No. 4.1; Matches 60: Conservative 52; Mismatches 93; Indels 81; Gaps 12; Qy 1 LQLMKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEK 56	RESULT 11  G64242  Cytadherence-accessory protein (hmwl) homolog MG386 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999 C;Accession: G64242 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C. Science 770, 397-403, 1995 A;Title: The minimal gene complement of Mycoplasma genitalium. A;Reference number: A64200; MUD:96026346
	A;Accession: G64242

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A;Note: the four fragments shown in reference A60991 correspond to four types of d with repeats ordered ABCCCDABCUDABCCCDABCDABC
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Best Local Similarity 20.3%; Pred. No. 45;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG----- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927 ITKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 TIETDPQTHQPVAVLGECASDPTSISLELDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Clostridium difficile toxin A; cpl repeat homology
                                                                                                                            R;Sauerborn, M.; von Eichel-Streiber, C.
Nucleic Acids Res. 18, 1629-1630, 1990
A;Title: Nucleotide sequence of Clostridium difficile toxin A.
A;Reference number: S08637; MUID:90221894
A;Accession: S08638
                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-55,'V',57-2079,'L',2081-2549,'S',2551-2710 <SAU>
A;Cross-references: EMBL:X51797
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                                                A; Cross-references: EMBL:X60984
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F; 2108-2128/Domain: cpl r
F; 220-2249/Domain: cpl r
F; 2201-2220/Domain: cpl r
F; 2242-2261/Domain: cpl r
F; 2315-2334/Domain: cpl r
F; 2315-2334/Domain: cpl r
F; 2335-2355/Domain: cpl r
F; 2377-2397/Domain: cpl r
F; 249-2468/Domain: cpl r
F; 249-2468/Domain: cpl r
F; 249-2468/Domain: cpl r
F; 249-2510/Domain: cpl r
F; 249-2510/Domain: cpl r
F; 256-2510/Domain: cpl r
F; 256-2502/Domain: cpl r
F; 2673-2672/Domain: cpl r
A; Molecule type: DNA
A; Residues: 1-92 <VON>
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F;1933-1952/Domain:
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R;Wren, B.W.; Clayton, C.L.; Tabagchali, S.
FEMS Microbiol. Lett. 70, 1-6, 1990
A;Title: Nucleotide sequence of Clostridium difficile toxin A gene fragment and detectid A;Reference number: A60991
A;Accession: A60991
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A; Residudes: '1',1884-1899,'K',1901-1910,'Y',1912-1919;2054-2074;2096-2116;2138-2158 <WRE
A; Cross_references: GB:X17194
R; Eichel-Streiber, C.; Laufenberg-Feldmann, R.; Sartingen, S.; Schulze, J.; Sauerborn, M
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Mol. Gen. Genet. 233, 260-268, 1992
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A;Accession: S22437
                                             A; Residues: 1'1616 <TIGR>
A; Cross-references: GB:U39723; GB:L43967; NID:g1046092; PID:g1046097; TIGR:MG386
A; Experimental source: strain G-37
C; Genetics: A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                              14;
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Description: Comparative analysis of Clostridium difficile toxins A and B. A; Reference number: S21894
A; Accession: S21897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ----LKASLDLL------TAVTIETDPQTHQPVAVL------GECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   632 PQEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDLSLELDSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :::||: | : | :|: | 518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQQEFSEPVVSDEKIKETNSDESVNTDL 577
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                                                                                                                                                                                                                                                                                           75; Indels 120; Caps
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                                                                                                                                                                                                                                                                                                                                           17 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVI,QKSSAWQLAKQK 76
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                                                                                                                                                                                                                                     8.5%; Score 104; DB 2; Length 1616; 20.6%; Pred. No. 23;
                                                                                                                                                                                                                                                                                        48; Mismatches
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                                                                                                                                                                                                                                                                                           63; Conservative
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A; Residues: 1-2710 <DOV>
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Best Local Similarity
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A; Residues: 1-154 <EIC>
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C. Species . Stanby Jordon aureus		
C.Date: 10-May-01-1000000000000000000000000000000000	QΩ	494 DAASKLLNTVEETT
C.Accession: F9000 R.Kuroda, M.; Obtta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud	Qy	127PVTANVTVAGPII
ma, A.; Mizucani-Ul, Y.; Nobayashi, N.; Sawano, V.; House, N.; Hattor, C.; Serimizu, N.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	qq	550 KDGSSKQKAMLEVHKTLF
Lancer 357, 122-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146	٥ مر م	181 SLSLLDKHSQIINKF
A;Accession: Fyoub/ A;Status: preliminary A:Molecule type: DNA	g ò	
A;Residues: 1-296 <kur> A;Cross-references: GB:BA000018; PID:913702563; PIDN:BAB43704.1; GSPDB:GN00149 A;Experimental source: strain N315</kur>	qa	 653 QLKHIFKISLIVADKIEC
Cjenels: SA2399 AjGene: SA2399	RESULT C82759	59 59 59 59
Query Match Best Local Similarity 25.5%; Pred. No. 2.6; Matches 53; Conservative 30; Mismatches 68; Indels 57; Gaps 10;	ZINC C;Sp C;Da C;Ac	zinc proceinase Aroaio Limpo C.Species: Xylella fastidios C.Date: 18-Aug-2000 #sequenc C.Accession: C82759
SETVONTL-KGILEKLKVDLGVLOKSSAWOLAKOKAQEAEKLLNNVISKLI.PTN-TU 	R;an Natu A;Ti A;Re	onymous, The Xylella fas re 406, 151-157, 2000 tle: The genome sequence ference number: A82515;
99	A;NO A;AC A;St A;St	A;Note: for a complete list A;Accession: C82759 A;Status: preliminary A;Molecule type: DNA
145	A;Re A;Cr A;Ex	sidues: 1-990 <sim> OSS-references: GB:AE005 perimental source: strai</sim>
	Brio	nes, M.R.S.; Nethach, ness, M.R.S.; Bueno, M.R. E.; Bocena, C.; El.
Db 246 ANELLKDNDELIASFSRALASDLRADQS 273	Subm A;Au J.D.	Submitted to Genbank, June A A;Authors: Ferreira, V.C.A.; J.D.; Junqueira, M.L.; Kempe
RESULT 14	chad A;Au	o, M.A.; Madeira, A.M.B. thors: Martins, E.M.F.;
G02157 Kinesin-like spindle protein HKSP · human C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001	Rodr A; Au	r. v.; Nubes, L.K.; Olivell Odrigues, V.; Rosa, A.J. d A; Authors: da Silva, A.C.R.; M.; Tsuhako, M.H.; Vallada,
C;Accession: G02157 R;Whitchead, C. submitted to the EMBL Data Library, September 1995	A; Re	ference number: A59328 ntents: annotation netics:
A;Reference number: NO0839 A;Accession: G02157 A;Status: preliminary; translated from GA/FMBI,/DDBJ	A : C	ne: XrO816
A;Molecule type: mKNA A;Residues: 1-1056 <wh1> A;Cross-references: EMBL:U37426; NID:g1171152; PIDN:AAA86132.1; PID:g1171153</wh1>	M Be	Query Match Best Local Similarity 2: Matches 54; Conservativ
C. Venderlus: A. Gene: GDB:RNSL1; Eq5; KSP A. Cross-references: GDB:13286; OMIM:148760	yo g	14 TGTSESLLDNLGNDLSNN::  : ::  ::
C;Superfamily: Kinesin-related protein Eg5; Kinesin motor domain homology C;Superfamily: Kinesin-related protein P-loop C;Keywords: ATP; nucleotide binding; P-loop F:19-36;JDomain: Kinesin motor domain homology <kmot> F:105-112/Region: nucleotide-binding motif A (P-loop)</kmot>	0	73 AKOKAQEAEKLLNNVISI 
Query Match 8.2%; Score 100.5; DB 1; Length 1056; Best Local Similarity 23.0%; Pred. No. 23;	Qy	132 VTVAGPIIGQIINLKASI :   : : 810 INVGNEAFGGTFSSRLN
vative 39; Mismatches 89; Indels 89; Ga	δλ	185 LDKHSQIINKFVNSV
Qy 21 LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 78	qq	:   :    :
Oy 79 E-AEKLENNVISKLEPTNTDIFGEKISNSLILDVKAEPIDDGKGENLSF 126	δλ	234 VVDNPQHKTQLQTL 247 :  : :

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Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froer, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La S.N.; Madelra, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. Ira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, G. M. A.; de Silva, V.E.; de Sa. R.G.; Santelli, R.V.; Sawa S. Ilva, R.; da Silva, A.M.; Silva, J.; M.A.; da Silva, F.R.; da Silva, A.M.; Silva, J.; W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3921; GB:AE003849; NID:99105710; PIDN:AAF83626.1; GSPDB:GN
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Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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GQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                  | :: | | | :| | | :: | GNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                                                                                                   ------VNSVINTLKSTVSSLLQKEICPLI----- 219
                                                                                                                                                                                                                                                                                         SQSLAAESKTVLQELINVLKTDLLSSLEMILSPTVVSILKINS 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of authors see reference number A59328 below
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orted] - Xylella fastidiosa (strain 9a5c)
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Db 916 IVRYERPDNYIUTL 929

Search completed: August 6, 2002, 17:05:12 Job time: 914 sec

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Q9np55 homo sapien
P42945 saccharomyc
007159 staphylococ
09utk5 schizosacch
49492 mycoplasma
P1614 clostridium
P52732 homo sapien
P43813 haemophilus
P93676 tomato mosa
P03587 Lomato mosa
P03587 tomato mosa
P5388 saccharomyc
P53076 saccharomyc
P53076 saccharomyc
O58718 methanococc
009459 caenorhabdi
005022 saccharomyc
P53075 methanococc
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1 LQLWKLVLLCGVLTGTSESL......NVIQQVVDNPQHKTQLQTLI 248
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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EGS_HUMAN
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RRPO_TOMK2
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YJK9_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weston W.M., LeClair E.E., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan K.S., Greene R.M.;
"Differential display identification of plunc, a novel gene expressed
in embryonic palate, nasal epithelium, and adult lung.";
J. Biol. Chem. 274:13698-13703(1999).
                                                                     62 GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSLILDVKAEPIDDG 119
                                                                                                                                       120 KGLNLSFPVTANVTVAGPIIGQ1INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 179
                                                                                                   51 ELLOQATSWPLAKNSILET---LNTADLGNLKSFTSLNGLLKINNLKVLDFOAKLSSNG 107
                                                                                                                                                              2 OLWKLVLLCGVLTGTSESLLDNLCNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                        180 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic organization of the mouse plunc gene and expression in the
                                                                                                                                                                                                                              progression (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- TISSUE SPECIFICITY: Upper airways, nasopharyngeal regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeClair B.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.;
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Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
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Biochem. Biophys. Res. Commun. 284:792-797(2001).
                                                                                                                                                                                                                                                                                                                                   278 AA.
                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE-21290678; PubMed-11396972;
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MEDLINE-99240770; Pubmed=10224143;
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MGI:1338036; Plunc.
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Higashiyama M., Yokouchi H., Ozaki K., Monden M., Tanigami A.;
"Isolation of a novel human lung-specific gene, LUNX, a potential
molecular marker for detection of micrometastasis in non-small-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LVLLCGVLTGTSESLLD-----S 29
POTENTIAL.
PROTEIN PLUNC.
4 X 6 AA REPEATS OF G.[LPQ]-[PL]-L-P-L.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
7F40BED9859188FB CRC64;
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Liu W.D., Zhou W., Wang L.;
                                                                                                                                                                                                                                                                                                                                                                                       15.7%; Score 192.5; DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 GILTKVLPELIQGKVCPLVNGILSGLDVTLVHNIAELLIHGLQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 NTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.6e-07;
                                                                                                                                 REPEAT 2.
REPEAT 3.
REPEAT 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21150203; PubMed-11251963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-20472055; Pubmed=11018263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     int. J. Cancer 91:433-437(2001).
                                                                                                                                                                                                                                                                                                     28611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             23.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_Tax1D-9606;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                         REPEAT
REPEAT
                                                                              DOMAIN
                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLUN_HUMAN
                                                                                                                                                                                                         REPEAT
                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                          RN BOUENCE FROM N.A.

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Balley J., Barlow K.F., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley O.P., Blid C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,

RA Clegg S., Cobley V.E., Garffiths M.D., Gwilliam R., Hall R.E.,

RA Elington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.M.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McWurray A.A.,

RA Minne S., Mistry D., Mocone M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Sydance B.J.C.T., Prathalingam S.R., Plumb R.W., Sims S.,

RA Sydance N., Sydance N., Taylor R., Teel., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudah M., Wallism S.A.,

RA Whitehead S.L., Whilteker P., Willey D.L., Williams S.A.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA Whitehead S.L., Whittaker P., Durbin R.M., Bentley D.R., Beck S.,

RA Whitehead S.L., Whittaker P., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lindahl M., Stahlbown B., Tagesson C.;
Lindahl M., Stahlbown B., Tagesson C.;
Lindahl M., Stahlbown B., Tagesson C.;
Identification of a new potential airway irritation marker, palate
"Identification of a new potential airway in human nasal lavage fluid with
two-dimensional electrophoresis and matrix-assisted laser
desorption/ionization-time of flight.";
Electrophoresis 22:1795-1800(2001).
-i- FUNCTION: May be involved in the airway inflammatory response
after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: Upper alrways and nasopharyngeal regions, including trachea and nasal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN PLUNC.
Q -> K (IN REF. 1; AAF70860).
; EDF152FBC35315BC CRC64;
"Cloning a new gene related to nasopharyngeal carcinoma."; submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 95-152; 157-167 AND 214-232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and some other types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBČELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21317946; PubMed=11425234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB024937; BAA93633.1;
EMBL; AF158745; AAF82622.1;
EMBL; AL121901; CAC03549.1;
EMBL; BC012549; AAH12549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF214562; AAG13653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 220 C 256 AA; 26712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF172993; AAF70860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar to the DALB0 gene, and a tRNA(Arg)."; yeast 11:873-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 SLIDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 78
                                                                                                                                                                                                                         131 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                 74 KOKAQEAEKLLNNVISK----LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                 78 KPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSPDGHRLYVTIPLGI 137
                                                                        14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                           45 TGLAGSLINALSNGL-----LSGGL------LG1LENLPLLDIL 77
                                       Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                  190 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                      197 PLPIOGELEDSLTGILNKVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 200.0 KDa protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%; Score 109; DB 1; Length 1769; 19.2%; Pred. No. 3;
14.9%; Score 183.5; DB 1; Length 256; 23.8%; Pred. No. 6.9e-07; tive 46; Mismatches 100; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1769 AA; 200080 MW; 064480D1D249B241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   redst il:0/3-003(1233).
-!- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
-!- SIMILARITY: CONTAINS 1 HEAT REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288C / FY1679;
MEDLINE=96090136; PubMed*7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0003645; YJL109C.
InterPro; IPR000357; HEAT_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X85021; CAA59385.1; ·· EMBL; Z49384; CAA89404.1; ··
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
REPEAT 1729 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 52; Conserva
                               Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YJE109C OR J0808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             YJK9_YEAST
P42945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                   Query Match
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                                                            132 VTVAGPIIGQ11NLKASLDLLTAVTIETD--PQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                          426 -----GELFEIRLITSLFINADVNTDIVKOLSDPV----FTTKKDIASFQTFLDKHS 473
                                                                                                                             -----KFVNSVINTLKSTVSSLLQKEICP 217
                                                                                                                                              ::11
474 ELINTINVSMLTETGERYKKŲLSLFTEAIGKGYKASSFLTSFFTTLESRITFLLRVT1SP 533
                             379 EVRLIITDLIYI.SEILEDKSQLVELFEYFISINEDLVLKCL-----KSLGLT----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
79 EAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 131
                                                                                                                                                                                                                                                                                                                                     01-0CT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 175:7495-7499(1993).
J. Bacteriol. 175:7497-7499(1993).
J. CATALIVIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
PATHWAY: SIXTH STEP IN GLYCOLYSIS.
J. PATHWAY: BELONGS TO CLASS 1 FRUCTOSE-BISPHOSPHATE ALDOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHIFF-BASE WITH DIHYDROXYACETONE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
295 AA; 32720 MW; A189E75574FIFCCO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00274; glycolytic_enzy; 1.
Probom; P0001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; FALSE_NEG.
Lyass; Schiff base; Glycolysis.
                                                                                                                                                                                                                                                                                                                 295 AA.
                                                                                                                                                                                                218 LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                              534 AAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 175:7495-7499(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000741; Aldolase_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94042930; Pubmed=8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kula M.R., Brockamp H.P.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus carnosus.
                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S33358; S33358.
PIR; A49943; A49943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P14223; 1A5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Goetz F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY
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INIT_MET
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"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil
"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil
Protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    151 -----LTAVȚIET------DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKF 195
                                                                                                                                                                                                                                                                        203 KKDQYVMLKLTIPTKVNAYSELJEHPOVIRVVALSGGYSRDEAN---KILKQNDGLIASF 259
                                                                                                                                                        111 VKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIIN---------LKASLD-- 150
                                                                         51 KGILEKLKVDLGVLQKSSAMQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 110
                                                                                                                                                                                              145 NNKEAIE--KVVKQQFEVAKEIIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 202
                                                                                                               93 KGIVPFLKVDKGLAEEADGVQLMK-PIPDLDKLLDRA-----NERGIFGTKM-RSNILE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,
CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and analysis of GFP-gene fusion library of fission
Match 8.6%; Score 106; DB 1; Length 295; Local Similarity 25.9%; Pred. No. 0.5; es 50; Conservative 31; Mismatches 64; Indels is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Fungi; Ascomycota: Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALM1_SCHPO STANDARD; PRT; 1727 AA. 09UTK5; 013313; 09UTR8; 16-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abnormal long morphology protein 1 (Sp8).
ALM1 OR SPAC1486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL133357; CAB62414.1; -.
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                                                                   196 VNSVINTLKSTVS 208
                                                                                                                                                                                                                                                                                                                                                                         260 SRALVSDLNAQQS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOKINESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-968 H90;
                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALM1_SCHPO
                                                           Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 GLKISNSLILDVKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 158
                                                                                                                                                                                                                                                                                                                                                                                                      449 -LETSNNNLTKVQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSR 507
                                                                                                                                                                                                                                                                                                                                                                                                                                        159 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 218
                                                                                                                                                                                                                                                                      333 SENSIRELQEKYDSVVSELQVVKENKNTSVSAGVGLFSPLAQKLSAVQNPEFSFTKVYSD 392
                                                                                                                                                                                                                                                                                                                                       393 NMKLQQKVSSLKLQLDRLINKFSSFCEQVKQRIPVVKQQRSEIVRNNIYMNFLSES---- 448
                                                                                                                                                                                                          61; Gaps
                                                                                                                                                                                                                                                                                                     49 --TLKGILEKLKVDLGVLQK--SSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIF 99
                                                                                                                                                                                                                                        17 SESLLDNLGNDLSNVVDKLEPV------48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
PEPERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                          DB 1; Length 1727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 175:7918-7930(1993)
-!- FUNCTION: COULD BE A ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE (BY SIMILARITY).
                                                                                                                                                                                       pred. No. 6.3;
41; Mismatches 94; Indels
                                                                                                                           F820BF8D9C132644 CRC64;
        COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPC00_MYCGE STANDARD;
049419; 049259; 049298; 049352; 049353;
01-NOV-1997 (Rel. 35, CreaLed)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                          8.5%; Score 104.5; C
24.3%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; Pubmed-7569993;
                               443 463 COLLE
804 1106 COLLE
1223 1427 COLLE
1497 1555 COLLE
1601 1664 COLLE
1727 AA; 197858 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 IRIFIHSL--DVNVIQQVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 LREKVRALECDVEIQKQTV 570
                                                                                                                                                                                                             63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma genitalium.
              361
463
740
1106
1427
1555
                                                                                                                                                                               Query Match
Best Local Similarity
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Coiled coil.
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between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQQEFSEPVVSDEKIKETNSDESVNTDL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 --IFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQI--IN---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 ----LKASLDLL------TAVTIETDPQTHQPVAVL------GECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 PQEGLEYKVOFLETEPKSLFDEKTIVVESEPPFIQPDLSLELDSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 SKEIKDSAKADLSNISDDIDSVWKEFGSFTOETQKSVEEKSQVDEILLDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                                                                                             17 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGTLEKLKVDLGVLQKSSAWQLAKQK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------KLLPTNTD----- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches 75; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1616;
                                                                                                                                                                                                Structural protein; Repeat; Complete proteome. 5 1389 2 x 32 AA REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=VPI 10463;
MEDLINE=90221884; PubMed-2109310;
MEDLINE=90221884; PubMed-5Lreiber C.;
Nucleotide Asquence of Clostridium difficile toxin A.";
                                                                                                                                                                                                                                                                                                        P -> S (IN REF. 2).
S -> F (IN REF. 2).
Mw; 6AF76A13AC49E4FF CRC64;
                                                                                                                                                                                                                                                           2 x 26 AA REPEAT.
2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-PEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   8.5%; Score 104; DB 20.6%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 AQEAEKLLNNVIS-------
                                                                                                                                      EMBL, U02245; AAA03401.1; ALT_FRAME.
EMBL, U02175; AAD12458.1; -...
EMBL, U02126; AAD12402.1; -...
                                                                                                                                                                                                                                                                                                                                         1616 AA; 185678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | :| |:||
| 692 ELN----HEELGNEFIN----
                                                                                                          EMBL; U39720; AAC71613.1; -. EMBL; U02245; AAA03400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20.6%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                  1236
1389
                                                                                                                                                                                                                                                                             11186
1339
256
304
                                                                                                                                                                                                                                                                389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KTQLQT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 TTQLET 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOXA OR TCDA.
                                                                                                                                                                                                       Cytadherence;
                                                                                                                                                                                     TIGR; MG386;
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P16154;
                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                DOMAIN
REPEAT
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TOXA_CLODI
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Kinesin-related motor protein Eg5 (Kinesin-like spindle protein HKSP) (Thyroid receptor interacting protein 5) (TRIPS) (Kinesin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E322F2141BEF1601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                            MEDLINE=98369052; PubMed-9701554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X85137; CAA59449.1; -. EMBL; U37426; AAA86132.1; -. EMBL; L40372; AAC41739.1; -. HSSP; P33176; 1BG2.
                                                                                                                                                                                                                                                 Cell 83:1159-1169(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363
480
764
1112
927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00129; KISC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          674 67
1057 AA;
                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLY PROPHASE)
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                      NCBI_Tax!D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
                                                        KNSLJ OR EG5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 148760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984 STSVKVQLY---AQLFSTGLNTIYDSIQLVN----LISNAVNDTINVLPTITEGI---- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  927 ITKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLI.N--NVISKI.LPTNTDIFG----- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 KTLLLDASVSPIPIKFILNNLKLNIESSIGDYIYYEKLEPVKNIIHNSIDDLIDEFNILEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                         Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
--- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833 AA REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF FIVE
                                                                                                                                                                                                                                                                                                 DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN ENTERACENTEROTOXIN CALLED A AND CYTOTOXIN B. ONLY AFTER THE ENTERAL DELIVERY OF THE ENTEROTOXIN A MAY THE CHARACTERISTIC DISEASE
                                                                                                                      Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 104; DB 1; Length 2710; 20.3%; Pred. No. 12;
                                                                                     Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 -PIVSTILDGINLGAAİKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                     CALLED PSEUDOMEMBRANOUS COLITIS BE INDUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EG5_HUMAN STANDARD: PRT; 1057 AA. P52732; Q15716; 01-572-1996 (Rel. 34, Created) 01-672-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1057 AA.
                 Nucleic Acids Res. 18:1629-1630(1990)
                                                                              MEDLINE-90129305; PubMed-2105276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002479; CW_binding.
Pfam; PF01473; CW_binding_1; 31.
Toxin; Enterotoxin.
                                                                                                                                                            Infect. Immun. 58:480-488(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X51797; CAA36094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X92982; CAA63564.1; -.
                                                                                                                                                                                                                                                                                          DIFFERENT OLICOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M30307; AAA23283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 20.3
Matches 56; Conservative
                                                                                                                                                                                                             STRAIN-VPI 10463;
von Eichel-Streiber C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508638.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                     SEQUENCE FROM N.A.
                                                                  STRAIN-VPI 10463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
EG5_HUMAN
1D EG5_HI
AC P5273;
DT 01-OCT
DT 01-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JI. Endocrinol. 9:243-254(1995).

FUNCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIPOLAR SPINCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIPOLAR SPINCLE. BLOCKING OF EGS PREVENTS CENTROSOME MIGRATION AND ARREST CLLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS.

SUBONIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE PRESENCE OF THYROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 819-868 FROM N.A. MEDLINE-95295737; PubMed=7776974; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- PTM: PHOSPHORYLATED EXCLUSIVELY ON SERINE DURING S PHASE, BUT ON BOTH SERINE AND THR-927 DURING MITOSIS, SO CONTROLLING THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING
                                                                                                                                                                                                                                                      Blangy A., Lane H.A., D'Herin P., Harper M., Kress M., Nigg E.A.; Phosphorylation by p34cdc2 regulates spindle association of human Eg5, a kinesin-related motor essential for bipolar spindle formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T->A: NO MITOTIC PHOSPHORYLATION, NO BINDING TO SPINDLE APPARATUS.
                                                                                                                                                         SEQUENCE FROM N.A., PHOSPHORYLATION SITE THR-927, AND MUTAGENESIS. MEDLINE-96128120; PubMed-8548803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead C.M., Rattner J.B.;
"Expanding the role of H8EGS within the mitotic and post-mitotic phases of the cell cycle.";
J. Cell Sci. 111:2551-2561(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSG0411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled coil; Mitosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY CDC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNS -> EL (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTIGERACY (196-512(1995).
Science 269:496-512(1995).
-i- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER
-i- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER
-i- FUNCTION: THIS PROTEIN AND 3' HYDROXYL GROUPS IN DOUBLE-
LINKAGES BETWEEN 5'- PHOSPHORYL AND 3' HYDROXYL GROUPS FOR
STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR
STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR
THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECURICE FROM N.A. ATCC 51907;
STRAIN-ED / KW20 / ATCC 51907;
STRAIN-ED / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Geoghagen N.S.M., Frinchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                         127 -----PVTANVTVAGPLIGQLINLKAS-LNLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                            181 SLSLLDKHSQ11NKF-------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 227
                                                                                                                                                                                                                                                                                                                               494 DAASKILNIVEE----TIKDVSGLHSKLDRKKAVDQIINAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                                                                          550 KDGSSKOKAMLEVHKTLFGNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                          E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 126
                                                                                                                                       447 LDQCKSDLQNKTQELE-----TTOKHLQETKLQL-VKEEV1TSALESTEEKIH 493
                                                                          70; Gaps
                                                                                                         21 LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGII,EKLKVDLGVLQK--SSAWQLAKQKAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
LIGN OR LIG OR HI1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILÁRITY: BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND KEPAL DAMAGED DNA (BY SIMILARITY).

CATALYTIC ACTIVITY. (ADOXYTIBORUTE ACTIVITY. NAD(+) + (deoxyribonucleotide)(N) + (deoxyribonucleotide)(N) = AMP + nicotinamide nucleotide + (deoxyribonucleotide)(N) = AMP + nicotinamide nucleotide + (deoxyribonucleotide)(N+M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus
                                         8.1%; Score 100; DB 1; Length 1057; 24.4%; Pred. No. 7.2;
                                                                             79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Mel. 32, Last sequence update) 16-OCT-2001 (Mel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679 AA.
                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
                                                                    24.48;
                                                                    Best Local Similarity 24.4%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                228 VN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                650 IN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNLJ_HAEIN
P43813;
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNLJ_HAEIN
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CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P89676; P90349;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biol. (Mosk) 31:826-830(1997).
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 VVIRRAGDVIPQII------GVLHERRPDNAKPIIF------PINCPVC----DS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 TLLNDVEFQVGRTGAITPVAKLEP--VFVAGVTVSNATLHNG-----DEIERLNIAIGDT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 KLLNNV------1SKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 NLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLGKSSAWQLA-KQKAQEAE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K.; Pelenovich E.V., Tructure of the tobacco mosaic virus strain K2 "properties and structure of the tobacco mosaic virus strain K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 QIINKFVNSVINTLKSTVSSLLQKEICPLIRIFI--HSLDVN-----VIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 QITRIEGEAVARCTGGLFCAAQRKE---ALKHFVSRKAMDIDGVGGKLIEQLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligase; DNA repair; DNA replication; NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 99; DB 1; Length 679; 23.1%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 23.1%; Pred. No. 4.8;
Conservative 41; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART: SM00278; HhH1: 2.
SMART: SM00532; LIGANC; 1.
PROSITE: PSS0172; HRCT; 1.
PROSITE: PS01055; DNA_LIGASE_N1; 1.
PROSITE: PS01056; DNA_LIGASE_N2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98012318; PubMed=9454068;
                                                                                                                                                                                                                                                                                                                             DNA_1igase_2BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00633; HHH; 1.
ProDom; PD003944; DNA_1igase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRCT.
                                                                                                                                                                                                                                                  DNA_ligase_N.
DNA_ligase_OB
                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam: PF00533; BRCT: 1.
Pfam: PF01653: DNA_11gase_N: 1.
Pfam: PF03120: DNA_11gase_OB: 1.
Pfam: PF03119: DNA_11gase_ZBD: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 23.1%;
                                                                               EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    [nterPro; 1PR003583; HHH_].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                    InterPro; IPR001357; BKCT.
InterPro; IPR001679; DNA_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00292; BRCT;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR004149;
InterPro; IPR000445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=138312;
                                                                                                                                                                                                                                                                                       InterPro; IPR004150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679 AA;
                                                                                                                                 1B04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION:
                                                                                                                                     087703;
HI1100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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-1. MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON DAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARCEL 1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein) (Contains: RNA-directed RNA helicase (MT/HEL) (126 kDa protein))
Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein);
Tomato mosaic virus (strain L) (TOMY) (TMY strain tomato).
Viruses; SSRNA positive-strand viruses, no DNA stage; Tobamovirus.
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J. Biochem. 96:1915-1923(1984).
-i- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 EEP-SIRGSMAKGELQLAGLSGDVPESSYTRSEEIBSLEQFHWATASSLJIKQMGSI--V 696
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Ohno T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002588; RNA_dep_RNApol2.
Interpro; IPR002588; V_methyltransf.
Interpro; IPR000506; Viral_helicasel.
Interpro; IPR000606; Viral_helicasel.
Interpro; IPR00043; RNA_dep_RNApol2.
Interpro; IPR000443; Viral_helicasel.
Interpro; IPR01660; Vmethyltransf; Interpro; IPR01660; Vmethyltransf; Interpro; 
-i- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON HAG OCCURS
BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
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20.4%; Pred. No. 16;
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-!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
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16-OCT-2001 (Hel. 40, Created)
16-OCT-2001 (Hel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence (EC 27.7.48) (183 kDa protein) (Contains: RNA-directed RNA polymerase (EC 27.7.48) (183 kDa protein) (Contains: PNA-directed RNA helicase (EC 27.7.48) (183 kDa protein))
Methyltransferase/RNA helicase (M/HEL) (126 kDa protein)).
Tomato mosaic virus (strain S-1) (TOMY).
Viruses: SRRNA positive-strand viruses, no DNA stage; Tobamovirus.
VILUSES: SRRNA positive-strand viruses, no DNA stage; Tobamovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                              Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding. CHAIN RNA-DIRECTED RNA POLYMERASE. CHAIN 1116 METHYLTRANSFERASE/RNA HELICASE. CHAIN
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W; A8EC8929B5CF7CAF CRC64;
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20.4%; Pred. No. 16;
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InterPro: IPR002688: V_methyltransf.
InterPro: IPR000606; Viral_helicasel.
Pram: PP00978: RNA_dep_RNApol2: I.
Pram: PF01443: Viral_helicasel: 1.
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1616 AA;
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Best Local Similarity
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"DNML, a dynamin-related gene, participates in endosomal trafficking
in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina: Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1 116 METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.0%; Score 98.5; DB 1; Length 1616; 20.4%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)

W; 5DBBFB2FADCC5C0C CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Dynamin-related protein DNM1 (EC 3.6.1.50).
DNM1 OR YLL001W OR L1381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches
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                                                                                                                                                                                                                                                                                        InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00978; kNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicase1; 1.
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MEDLINE-96405918; PubMed=8810043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Biol. 130:553-566(1995).
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                                                                                                                                                                                                                              EMBL; AJ132845; CAH36997.1; -.
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                                                                                                                                                                                                                                                                  EMBL; AJ132845; CAB36998.1;
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1616 AA;
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P54861;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 SESLKLAREVDPOGKRTIGVITKLD-LMDSGTNALD-ILSGKMYPLKLGFVGVVNRS--- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QLAKQKAQEAEKLLNNVISKLLPTNTDIF-------GLKISNSLILDVKAEPID 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SESL-----LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD-LGVLQKSSAW 70
                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-OST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 97; DB 1; Length 757; 23.1%; Pred. No. 7.8; tive 35; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H -> ISPD (IN REF. 1);
; EBEF8793C5951770 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 NESRASLV---LQLMNKFSTNFISSIDGTSSDINTKELCGGARIY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SPUCATOR GED; L. SMART; SMOODS, GED; L. SMOOTS, SMOOTS, SMOOTS, DYNAMIN; 1. Hydrolase; Motor protein; GTP-binding, 42 GTP (POTENTIAL). GTP (POTENTIAL). GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 124 H
757 AA; 84971 MW;
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InterPro; IPR001401; Dynamin.
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Pfam; PF02212; GED; 1.
                                                                                                                                                                                                                                                                                                 EMBL; L40588; AAA99998.1; -.
                                                                                                                                                                                                                                                                                                                X91488; CAA62769.1; -. Z73106; CAA97444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00350; dynamin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.1% les 52; Conservative
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SMART; SM00053; DYNC; 1.
SMART; SM00302; GED; 1.
                SEQUENCE FROM N.A.
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P53076;
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NCBI_TaxID-4932;

N CBI_TaxID-4932;

N CBI_TaxID-4932;

P SEQUENCE FROM N.A.

Fartmann B., Kramer W.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

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R EMBL: 27249; CA49643.1;

R SGD; SO003196; V1D30.

R InterPro: IPR003878; SPRY.

R InterPro: IPR003878; SPRY.

R MATERPOOR IPR003878; SPRY.

M Hypothetical protein.

T DOMAIN 165 185 POLY-ASP.

O SEQUENCE 958 AA; 108178 MW; 335ADDIS2949FBC8 CRC64;
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iearch completed: August 6, 2002, 17:07:32
'ob time: 874 sec

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Q63471 rattus norv
Q63550 rattus norv
Q96hk6 homo sapien
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O9d6p2 mus musculu
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Q9cqx3 mus musculu
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Q9bqp8 homo sapien
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385.296 Million cell updates/sec
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Q96dr5 homo sapien
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bos taurus
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                                                                                                                                 1 LQLWKLVLLCGVLTGTSESL.....NVIQQVVDNPQHKTQLQTLI 248
                                                               August 6, 2002, 17:09:28; Search time 111.35 Seconds
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                                                                                                                                                                                                            562222
GenGore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                       562222 seqs, 172994929 residues
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Listing first 45 summaries
                                            OM protein - protein search, using sw model
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P79125
Q9D734
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Q9D794
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09D9J8
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Q9SMV6
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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: sp_bacteria:*
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099110 Comato mosa 069135 mus musculu 059040 methanococc 09xu2 caenorhabdi 09yng5 tobacco mos 09ja04 tobacco mos 09ja04 tobacco mos 09bjy0 plasmodium 061351 mus musculu 049948 mycoplasma 09dut4 porcine rub 061769 mus musculu 061769 mus musculu 061769 mus musculu 061769 mus musculu
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Q9pf62 xylella fas
Q77136 apis mellif
Q54416 staphylothe
Q9cf11 lactococcus
Q9c2c8 neurospora
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099u54 staphylococ
0931r6 staphylococ
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Q99tnO staphylococ
             rattus ratt
                      staphylococ
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Q9n218 caenorhabdi
Q9ks47 vibrio chol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tracey A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121901; CAC03546.1; -.
SEQUENCE 249 AA; 27011 MW; E64E0794A1B4DB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49G10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30).
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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Q9XTU2
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Q9PF62
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Q61769
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NCB1_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haigh B.J., Wilkins R.J., Wheeler T.T.; The cloning and sequencing of two cDNAs coding for alternate forms of
                                                                                                                                                                                                                                                                                                       Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (ACT-2011). AAL28113.1;
SEQUENCE 249 AA; 27110 MW; FD54B624AlA4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LGVLQKSSAWQLAKQKAQEAEKIJINNVISKLI,PTNTDIFGLKISNSI,LLDVKAEP1DDGK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GLNLSFPYTANVTVAGPIIGOIINLKASLDLLTAVTIETDPQTHQPVAVLRECASDPTSI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLJLDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVT!FTDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SISELDKHSQIINKFVNSVINTLKSTVSSILQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
182 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEJCPLIRIFIHSLDVNVIQQVVDNPQH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LQLWKLVLLCGVLTGTSESLLDNIGNDLSNVVDKLEPVLHEGI.ETVDNTLKGTLEKI.KVU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                99.3%; Score 1220; DB 4; Length 249; 99.6%; Pred. No. 1.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                            PRT;
                                                                                                                                                                                               PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 KTQLQTL1 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 KTQLQTLI 249
                               241 KTQLQTLI 248
                                                        242 KTQLQTLI 249
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB1_TaxID=9913;
                                                                                                                                                                                                                                                                                               TISSUE=PAROTID;
                                                                                                                         Q96DR5
Q96DR5;
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96DR5
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Haigh B.J., Wilkins R.J., Wheeler T.T.; "The cloning and sequencing of Lwo cDNAs coding for alternate forms of WSP30, a bovine member of the Parotid Secretory Protein family."; submitted (NOV-1966) to the EMBL/CenBank/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 --- LESRCSDEVVEQ--QETENFLEQLISRIFQVVSRLTGVRIRNVQVPDITFEATSENS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SI.SLLDKHSQIINKFVNSVINTI.KSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS1 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 A-DVSIPITADVTVSLPLLGEIVKLDLNVDLQTSVSIETDAETGDSRVVVGECPNNPESI 173
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  2 VQLWKLVLLCGLLAGTSESLLDIRGND---VLRRLISGLERGLGTFDSTIEI1FQNLKTE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1.QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLWKLVLLCGLLAGTSASL,PDIRGND---VLRKLKSGLERGLDTFDSTIEIIFQNLKTE 58
                                                                                                                                                                                                                                                                                                                                                     1 LQLWKLVILLCGVLTGTSESLLDNIGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKI.KVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
BSP30, a bovine member of the Parotid Secretory Protein family."; Submitted (NOY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79413; AAB38282.1; -. SEQUENCE 243 AA; 26877 MW; OC2DBDD45660E11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%; Score 415.5; DB 6; Length 240; 37.9%; Pred. No. 7.8e-23; tive 56; Mismatches 84; Indels 11;
                                                                                                                                                                                                          Query Match 35.6%; Score 437; DB 6; Length 243; Best Local Similarity 38.6%; Pred. No. 2.1e-24; Matches 95; Conservative 58; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U79414; AAB38283.1; -.
SEQUENCE 240 AA; 26513 MW; 850611DE9E43E358 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                     95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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SIĞNAL 1 20 PC
CHAIN 21 235 NI
SEQUENCE 235 AA; 24529 MW;
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EMBL; M83209; AAC06334.1; -.
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                                                                                                                                 Rattus norveqicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mirels L., Ball W.D.;
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Matches 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98129760;
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                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                multigene family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CSTBL/63; TISSUE-TONGUE;

RX Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinaqawa A., Shibata K., Konno H., Adachi J., Frkuda S., A Lawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Lazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rabischmann W., Casavant T., Rasikawa T., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Rasika K., Sakai K., Okido T., Futuno M., Anno H., Baddarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Romstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anno P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinshaw Bootis A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L., Manachizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.
171 SLTVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDAECVEKLIGESQD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 KSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSL1LDVKAEPIDDGKGLN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 QATSWPLAKNSILET---LNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSSNGNGID 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 LSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LVLLCGVLTGTSESLLDNLCNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LVVLCGLLIGNSESLLGELGSAVNN------LKILNPPSEAVPQNLNLDVELLQ 54
                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Finctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 LLDKHSQIINKFVNSVINTLKSTVSSLLQKEJCPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%; Score 352.5; DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA; 24737 MW; A29D0160268DA0CF CRC64;
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%; Pred. no.
                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLEEL 17, 01-JUN-2001 (TrEMBLEEL 17, 01-JUN-2001 (TrEMBLEEL 17,
                                                                                                                                                                                                                                                                                        PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
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                                                      241 KTQ 243
                                                                                            231 TTQ 233
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                                                                                                                                                                                                            Q9D734;
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RESULT 6 Q63471 ID Q63471

Matches

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Mirels L., Ball W.D.;
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy
protein are alternatively regulated members of a salivary protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PECURSOR.
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MEDLINE-92129360; PubMed-1370829;
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MEDLINE-92129360; PubMed-1370829;
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PRELIMINARY;
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                                                                                                                                                                                232 QQV 234
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"Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                          58 KVDLGVLQKSSAWQLAKQKAQEAFKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID 117
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Best Local Similarity 23.9%; Pred. No. 0.00098;
Matchiz 58; Conservative 48; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                47; Gaps
                                                                                                                                                                                                                                                                                                                         4 WKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKI,KVDL 61
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                                                                                                                                                                             POTENTIAL.
NEONATAL SUBMANDIBULAR GLAND PROACINAR
CELL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       16.9%; Score 207.5; DB 11; Length 206; 24.0%; Pred. No. 9.6e-08;
                                                                                                    Mirels L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland Bl-immunoreactive
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01-DEC-2001 (TrEMHLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO DNA SEGMENT, CHR 2, MASSACHUSETTS INSTITUTE OF
TECHNOLOGY 19.
                                                                                                                                                                                                                                                                               84; Indels
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EMBL; BC008429; AAH08429.1; -
SEQUENCE 484 AA; 52427 MW; 08242B697284E858 CRC64;
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                                                                 SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                               53; Mismatches
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                                       Biol. Chem. 267:2679-2687(1992)
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EMBL; M83210; AAC12783.1; -.
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16.9%
Best Local Similarity 24.0%
Matches 58; Conservative
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                                                                                          MEDLINE-98129760;
                            multigene family.
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102 TYNQELVVRIPLDMVAGLNTPLIKTIVEFQMSTEVQALIRVERSKS--GPAHLNLSDCSS 159
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                                                                      62 -----GVIQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                                               116 IDDGKGLNLSFPVTANVTVAG --- PIIGQIINLKASLDLLTAVTIETUPQTHQPV-AVLG 171
                                                                                                                                                                                                                                                                                                                                                                                 172 ECASDPTSISUSLIDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIKIFIHSLDVNVI 231
                                                                                                                                                 45 KDHNATSILQQLPLLSAMREKPAGGIPVLGSLVNTVL---KHVIWLKVITANILQLQVKP 101
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 WKLVLLCGVLTGT-----SESLLIDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 WILTELEGELLGATEVQANYPPAVL-NEGPEV-----IQKHETQAEKDHDAT--AJLQE 55
5 WTFTLLCGLLAATL...--POATLSPTAVLILG-----PKVIKEKLTOEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 150.5; DB 11; Length 474; 23.1%; Pred. No. 0.004; Live 56; Mismatches 84; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA; 52373 MW; 377DBFA5E736709B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 DPTSISLSLI, DKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 NESTLRLSLLHKLSFVVNSLAKNVMNLLVPALPQIVKNHLCPMIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VON EBNER MINOR SALIVARY GLAND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
U-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310074B19R1K PROTEIN.
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InterPro: PRROIL12; LBP_BPI_CETP.
SMART; SM00328; BPII; 1.
SMART; SM00329; BPI2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.1%
Matches 52; Conservative
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Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-Fr,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                 Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kiyosawa H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Salto T., Okazaki Y., Globori T., Bono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Puruno M., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LELSVKLDVTAEVYAVRDSYGRSKL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J: TISSUE-TONGUE;

REDLINE-2186560; PLDMed-1217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Rono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 148.5; DB 11; Length 235; 25.3%; Pred. No. 0.0023;
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SEOUENCE 235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel 17, (TrEMBLrel 17,
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                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2310021H06RIK.
2310074B19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kishoo B., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakani K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Remister M.J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriff L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Fluruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Pletcher C., Fulita M., Gariboldi M., Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshell S., Lander B., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 LELSVKLDVTAEVYAVRDSYGRSRL-VJGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 VLGKVISS-IPLLNNILDIRVINPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Subaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia: Eutheria; Kodentia; Sciurognathi; Muridae; Murnae; Mus.
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                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 148.5; DB 11; Length 270; Best Local Similarity 25.3%; Pred. No. 0.0027; Matches 39; Conservative 38; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                            FULLY 409:685-690(2001).
EMBL; AKOO9441; BAB26290.1; -.
BMGD; MGI:1914385; 2310021H06Kik.
GFOHFNCE 270 AA; 29223 MW; DB63327561D910AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 270 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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PRT;
                                                                                                               39; Conservative
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                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                  Matches
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X MEDLINE-21085660: Pubmed-11217851;
X MANAI V. Shinada W. Shibata K. Koshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ruchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrim L. M., Staubi F., Suzuki R., Pomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
Blownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbadh C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 JNLKASLDLLTAVT1ETDPQTHQPVAVLGECASDPTSISLSLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148.5; DB 11; Leus...
pred. No. 0.0027;
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                                                                                                                                                                                                                                                                                                                                                          29175 MW; 492A16EEBAB4A677 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 LTRVIPGLVQCVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 LKSTVSSLLQKEJCPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches
Nature 409:685-690(2001).
EMBL; AK010115; BAB26710.1; -
EMBL; AK009319; BAB26521.1; -
EMBL; AK009531; BAB26543.1; -
EMBL; AK009562; BAB26340.1; -
EMBL; AK009562; BAB26372.1; -
EMBL; AK009595; BAB26471.1; -
EMBL; AK009803; BAB2644.1; -
EMBL; AK009803; BAB2644.1; -
EMBL; AK009803; BAB26513.1; -
EMBL; AK009803; BAB26513.1; -
EMBL; AK010912; BAB26543.1; -
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MGD; MGI:1914385; 2310021H06Rik.
                                                                                                                                                                                                                                                                                                      EMBL; AKO10051; BAB26667.1; -.
MGD; MGI:1914385; 2310021H06Kik.
SEQUENCE 270 AA; 29175 MW; 4
                                                                                                                                                                                                                                                AK009835; BAB26533.1; -. AK010012; BAB26642.1; -. AK010051; BAB26667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 AA;
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              LERKKKKKKKKKKO
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RECEIVE. TISSUE-TESTIS;

REDLINE-21085660; PubMed=11217851;

R RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

R RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukuhishi Y., Konoo H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa H.A., Ashburner M., Batalov S., Casavant T.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Schriml L.M., Staubli F., Suzuki R., Tomitan M., Magner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Anno H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Browstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

RA Sakai M., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schopabach C., Sebrandto N.,

RA Sasaki H., Sato K., Schopabach C., Schoza T., Shibata Y., Storch K.-F.,

RA Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                         83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                     108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVÖSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                   143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
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Best Local Similarity 21.1%; Pred. No. 0.036;
Matches 55; Conservative 54; Mismatches 88; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 KG-----ILEKLKVDLGVLQKSSAWOLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LWK-LVLLCGVLT------GTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTL 50
                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LWRLLVLLLGLLALPSALPKQPWPGLTKAHKDGRST-----LARIIAQGLLKLN--A 53
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoslomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL: AROUGESS: BAB24760.1.
MGD: MGI:1920638: 1700058C13Rik
11.8%; Score 145.5; DB 11; Length 270; 25.3%; Pred. No. 0.0045; Live 38; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AA; 25713 MW; 0D52D24A3076D5DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1700058C13RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
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./ 105 NSLILDVKAEPIDDGKGLNLSFP---VTANVTVAG------PIIGQIINLKASLDLLTAV 155

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62 -----GVLUKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 SANDQELLVKIPLD -- - MVAGFNTPLVKTIVEFHMTTE -- AQATIRMDTSASGPTRLVLS 156
156 TIETDPQTHQPVAVLGECASDPTSISLSL-LDKHSQIINKFVNSVINTLKSTVSSLLQKE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 IDDGKGUNLSFPVTANVTVAG---PIIGQIINLKASLDLLTAVTIFTDPQTHQPV-AVLG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
10.5%; Score 129; DB 4; Length 199;
Best Local Similarity 24.2%; Pred. No. 0.049;
Matches 54; Conservative 40; Mismatches 89; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 WIFTLICGLLAATL------IQATESPTAVILG------PKVIKEKLTQEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WKLVLLCGVLTGTSESLLDNLCNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrcl. 17, Created)
01-JUN-2001 (TrEMBLrcl. 17, Last sequence update)
01-DEC-2001 (TrEMBLrcl. 19, Last annotation update)
BA49G10.6 (SIMILAR TO MURINE VON EBNER MINOR SALIVARY GLAND PROTEIN, ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracey A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL121901; CAC03550.1; -.
NON_TER 199 199
SEQUENCE 199 AA; 21517 MW; 49A4CC2143BE04B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 ECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKE 214
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                                                                                                                                                                              :|||| : ||| : ||
208 VCPLIGEILRQIDVKLLKGLV 228
                                                                                                                                                 215 ICPLIRIFIHALDVNVIQQVV 235
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                          Q9BQP8
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Q9BQP8
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Search completed: August 6, 2002, 17:09:28 Job time: 930 sec

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August 6, 2002, 16:52:51; Search time 138.55 Seconds (without alignments) 198.818 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                             1 LQLWKLVLLCGVLTGTSESL......NVIQQVVDNPQHKTQLQTLI 248
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human parotid secr Human Parotid secr Human Parotid secr Human secreted pro Human secreted pro Human protein sequ Peptide #8941 enco Human bora marrow Peptide #9264 enco Mouse 28.6 kba sec
D	AAW69221 AAB24069 AAB24069 AAB25765 AAB75351 AAB75351 AAB76336 AAM75311 AAM52308 AAM35227
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Result.	11 10 10 11

(HUMA-) HUMAN GENOME SCI INC.

Duan R, Ruben SM;

97WO-US23522. 96US-0034429.

18-DEC-1997; 23-DEC-1996;

02-JUL-1998

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Z >	WO9828420-A1	8420-,	A1.	ŀ				

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WPI: 1998-377651/32.

N PSDB: AAV44759.

New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening

Claim 16; Fig 1: 94pp: English.

This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to atsess the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
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Sequence 249 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal tissue; HSPSP, Sjorgen's syndrome; draves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                       121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                        181 SI,SLLDKHSQIINKFVNSVINTI,KSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
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                                                    0; Gaps
                                                                                                 1 LOLWKLVLLCGVIJGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                           2 lqlwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkvd 61
100.0%; Score 1228; DB 19; Length 249; 100.0%; Pred. No. 2.3e-100; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW60682 standard; Protein; 249 AA.
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                                                    Matches 248; Conservative
     Query Match
Best Local Similarity
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WO9821329-A1.

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purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autolimune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTUIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SLSLLDKHSQJINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 lglwklyllcgvltgtseslldnigndlsnvvdklepvlhegletvdntlkgileklkvd 61
                                                                                                                                                                                                                                                                                                   New parotid secretory protein · useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1228; DB 19; Length 249; Best Local Similarity 100.0%; Pred. No. 2.3e-100; Matches 248; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1A-C; 65pp; English.
                                                             97WO-US20651
                                                                                                          96US-074928B.
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                                                                                                                                                     (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                             Goli SK;
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                                                             07 - NOV - 1997;
                                                                                                     14-NOV-1996;
                     22-MAY-1998.
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- A THEOTON --

1 LOLWKLVLIGGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60

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Human; tumour; diaquosis; neoplastic disease; neoplastic cell growth;
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                                                                                                                                                                                                                                proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disorder; immunologic disorder.
                                                           Human PRO1025 protein sequence SEQ 1D NO:38.
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99WO-US30911.
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99US-0141037.
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Wood WI;
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25-JUN-1999;
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                                                                                                                                                                                                                                     The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO30, PRO311, PRO535, PRO619, PRO1031, PRO105, PRO105, PRO1050, PRO2198, PRO319, PRO1151, PRO1152, PRO1184, PRO2198, PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treated without compounds and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified artibodies and other compounds include benign or malignant tumours controlled and cher proceed. Prosectal, prostate pancreatic, lung, vulva, thyroid hepstic carcinomas, sarcomas, globlastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, epithelial, stronal and blastocoedic disorders, and inflammatory, angiogenic and immunologic disorders. AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC5836 and AAB24089 represent human PRO PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1228; DB 21; Length 249; 100.0%; Pred. No. 2.3e-100; tive 0; Mismatches 0; Indels 0;
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mes 248; Conserva
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Query Match Matches

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chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAART25.A8774 which encode human secreted proteins AAB25563-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                     61 I.GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                         121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                     181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                         2 iqiwklvilicgvltgtseslidnigndlsnvvdklepvlhegletvdntlkgilekikvd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                         AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein SEQ ID #77.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       septic shock; impotence.
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                                                                                                                                                                                                                                                                            241 KTOLOTLI 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB25765;
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                                                                                                                                                                                                                                                                                                                                                                       RESULT
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proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmue diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
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249 AA; Sequence

248:

Query Match Best Local Si Matches 248;

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The present invention relates to 49 Secreted proteins and the CDNAS
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorder.
                                                                                                                                               Local Similarity
                                                                               249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 KTQLQTLI 248
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                                                                                                                                                                 248;
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                                                                                 Sequence
                                                                                                                               Query Match
                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                 121 GLALSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                 2 Iglwklyllcgyltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkvd 61
                                                                                                                                                                                                                                                                               1 LQLWKLVLLCGVLTGTSESLLDNI,GNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                            100.0%; Score 1228; DB 21; Length 249; 100.0%; Pred. No. 2.3e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                             :0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001 (first entry)
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                             Local Similarity
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49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -

Claim 10; Page 281; 307pp; English

Jobert S;

Dumas Milne Edwards J, Bougueleret L,

(GEST ) GENSET

21-DEC-1999;

04-JAN-2001.

infection

AAB75351;

.B75351

WPI; 2001-071487/08

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antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiagqregant; haemostatic; vulnerary; antiuloer; osteopathic; eczema; dermatological; antialaregic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antiamaphylactic; rheumatoid arthritis; septic shock; pancreatiits; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                             61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                      121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 glnlsfpvtanvtvagpiigqiinlkasldlltavtietdpqthqpvavlgecasdptsi 181
                                                                                                                                                                                                                                                              1 LOLWKILVILEGGVLTGTSESLLDNIGNDLSNVVDKLEPVLHEGLETVDNTLKGJLEKLKVD 60
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                        2 ]qlwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkvd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1228; DB 22; Length 249; 100.0%; Pred. No. 2.3e-100;
                                                                                                                                                                                                                 Indels
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0
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinifiammatory; antirheumatic; cells they are expressed in, such as: antinifiammatory; antirheumatic; cells they are expressed in, such as: antinifiammatic; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; cardianeamic; antiagraphy andiactic; unmunosuppressive; antiagraphy antiagraphmatic; untilders antiagraph, antiagraphmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotectides are useful for screening for production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, reunopathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, barmacopical disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic incurological disorders, cancer, multiple sclerosis, depression, heurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GLNLSFPVTANVTVAGPIIGQIINLKASUDILTAVTIETDPQTHQPVAVIGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGTLEKLKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1190; DB 22; Length 260;
Pred. No. 5.5e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                 Claim 20; Page 260; 1217pp; English.
Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.98;
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                                              2001-457603/49.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AA;
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253 ktqlqtli 260
                                                                    N-PSDB; AAH99686
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Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.1e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                  21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                         26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207456. 30-JUN-2000; 2000US-0608408.
                                                                          30-JAN-2001; 2001WO-US00669.
                                                                                                          04-FEB-2000; 2000US-0180312.
                                                                                                                                                      03-AUG-2000; 2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; cancer.
             WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157275-A2.
                                                                                                                          26-MAY-2000;
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                                              09-AUG-2001
                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Human; foetal liver; gene expression; single exon nucleic acid probe.

Homo sapiens.

Peptide #8941 encoded by human foetal liver single exon probe.

04-FEB-2002 (first entry)

ABB41435;

ABB41435 standard; Peptide; 50 AA.

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(BB41435 RESULT.

Penn SG,

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Gaps

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and dissplaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #9264 encoded by probe for measuring placental gene expression.
                                                              The present invention provides a number of single exon nucleic acid
                        Example 4; SEQ 1D NO: 35417; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                       137 PIIGUIINLKASLDLLTAVTIETDPOTHOPVAVLGECASDPTSISLLLD 186
                                                                                                                                                                                                                                                                       Length 50;
                                                                                                                                                                                                                                                                                                                                                                         1 pliggiinlkasldlltavtietdpgthqpvavlgecasdptsislslld 50
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                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                     20.0%; Score 246; DB 22;
100.0%; Pred, No. 1.1e-14;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM35227 standard; Protein; 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
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21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0236359.
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                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53.
                                                                                                                                                                                                           50 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM35227;
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              × 8 × 0 0 0 0 0 0 0 × 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                       Example 4; SEQ 10 NO: 34413; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.1e-14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                           DR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                           Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM75111 standard; Protein; 50 AA
                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen w,
                                                         04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the probes of the invention.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456.
2000US-0608408.
                                   2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200005-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
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20;

Matches

Query Match

AAM75111;

SULT M75111

Sednence

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The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration and proliferation. Cell-cell interaction and the differentiation of tissue specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful in genome and physical mapping, in positional cloning of are useful in genome and physical mapping, in positional cloning of creatment of mammalian diseases. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response treatment, as immunoregularcry and anti-inflammatory molecule, as diagnostic for specific types of cancer readment, as target for antagonists in the treatment of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block the invention, and as anti-inflammatory and/or vaccine adjuvant.

The present sequence is 28.6 kba protein, a secreted protein from mouse.
                               ó
                                                                                                                                                                                                                                                                                                                                                                                    Mouse, cytostatic; antiinflammatory; immunoregulatory; tissue integrity; wound healing; immune response; vaccine; caucer; asthma; allergy; cell trafficking; therapy; 28.6 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -
                               Gaps
                               0
                                                                     137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                         1 piigqiin|kas|dlltavtietdpqthqpvavlgecasdptsis|s||d 50
                             Indels
                             ..
           Pred. No. 1.1e-14;
100.0%; Prec. ....
                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 92; 101pp; English.
                                                                                                                                                                                                                                                                                                                                              Mouse 28.6 kDa secreted protein.
                                                                                                                                                                                                                    AAE05367 standard; Protein; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0171678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2000; 2000US-0724864.
                                                                                                                                                                                                                                                                                                   12-SEP-2001 (first entry)
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson JD, Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WP1; 2001-425665/45.
           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD10135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200148192-A1.
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                                                                                                                                                                                                                                                               AAE05367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
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143 INLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLDKHSQIINKFVNSVI 200
                                                                                                                                            67 nptdllagkítdalsggl-----lsggl-----lgileniplldviksgggnsnglvg 114
                                                                                                                                                                       86 NVISKL---LPTNTDIFGLKISNSI,ILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                             Gaps
                                                                                   7 lvvicgllahstaqlaglplplgqgpplplnggpplplnggqllplagglplavspalps 66
                                                                                                               30 NVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a novel human secreted protein, termed nh/396.1. The sequence is predicted from a full-length CDNA clone (see AAX59356) isolated from a human adult brain (thalamus) CDNA lbbrary. The invention provides CDNA clones (see AAX59352-58)
                             61;
 Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; nh796_1; human; brain; thalamus; therapy;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "predicted leader/signal seguence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LaVallie ER;
                                                                                                                                                                                                                                                                                     201 NTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                     231 giltkvlpeliggkvcplvngilsgldvtlvhniaellihglg 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding secreted human proteins
DB 22;
                             49; Mismatches 107;
                                                          6 LVLI,CGVLTGTSESLLD------NLGNDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K, LaVa
r RJ, Treacy M;
15.4%; Score 189.5; DB 2
23.3%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steininger RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       AAY06408 standard; Protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US27903.
             23,3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC.
                           66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-419350/35.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX59356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09935252-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06408;
                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                             Matches
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       131 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 KOKAQEAEKI,LNNVISK---LLPTNTDIFGI,KISNSLILDVKAEPI,DDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 kpgggtsggllggilgkvtsvipglnniidikvtdpqllelglvqspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 klqvntplvgasllrlavklditaeilavrdkgerihl-vlgdcthspgslqislldglg 196
                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches 100; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 tglagsltnalsngl-----lsggl-----lgilenlplldil 77
encoding novel secreted proteins (see AAY06404-10) of the human testis, brain and foetal kidney. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell proliferation or differentiation, immunostimulatent (e.g. as vaccine) or immunosuppressive, haematopoiesis regulating, tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New LS170 nucleic acid from lung tissue – useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.9%; Score 183.5; DB 20; Length 256; Best Local Similarity 23.8%; Pred. No. 3.2e-08;
                                                                                                                                                                                   growth, activin or inhibin, chemotactic or chemokinetic, haemostatic, thrombolytic, receptor/ligand, antiinflammatory, cadherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedman PN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colpitts TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dosen, Hodges SC, Klass
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US11601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LS170 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-060335/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts-rapp L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX00809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1997;
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                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95463;
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                       contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polynucleotide that comprises the treating a test sample with at least one LS170 specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LS170 gene. The LS170 overlapping sequences trepresent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease, specifically cancer, and to indicate predisposition to such disease, particularly detection of LS170 polynucleotide. LS170 antigons, or anti-LS170 antibodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in assays; as targets for drug screening, and scomponents or targets for therappy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can be used to deliver therapeutic agents to LS170-expressing cells; directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 KQKAQEAEKI,LNNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 kpgggtsggliggligkvesvipglnniidikvtdpglielglvgspdghrlyvtiplgi 137
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Sequences AAW95463-471 represent LS170 polypeptide fragments which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macina RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0095233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (first entry)
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WP1; 2000-195589/17.
N-2SDB; AA261165.
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Lung specific genes for developing products for diagnosing, monitoring, staging, prognosticating, imaging and treating lung cancer

Example 2; Page 35-36; 37pp; English.

The present sequence is encoded by a lung specific gene, designated Lng110, clone ID 135520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer, especially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for treating lung cancer.

Sequence 256 AA;

Query Match 14.9%; Score 183.5; DB 21; Length 256; Best Local Similarity 23.8%; Pred. No. 3.2e-08; Matches 56; Conservative 46; Mismatches 100; Indels 33; Gaps 6;

74 KQKAQEAEKLINNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130

SSULT 15 \U39019

AAU39019 standard; Protein; 256 AA.

AAU39019;

16-JAN-2002 (first entry)

Human secreted protein nh796\_1.

Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimiorobial; vulnerary; cytostatic; antidiabetle; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antiumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; Still; tumour; autoimmune disorder; multiple sclerosis; rhemmatoid arthritis; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; huntington's disease; infection; cardiac disease; stroke, sepsis; inflammatory bowel disease; contraceptive; immunogen; food supplement; vaccine.

Homo sapiens.

WO200175068-A2.

11-OCT-2001.

Search completed: August 6, 2002, 16:52:52 Job time: 334 sec

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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation activity or may induce production of other or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined communed ficiencies and disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, and shy-brager syndrome, infections, and shy-brager syndrome, infections, and infartion of cardiac and central nervous system vessel e.g. stroke, and infartion of icardiac and central nervous system vessel e.g. stroke, and infartion of icardiac and central nervous system vessel e.g. stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                       Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and
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7, Steininger RJ, Spaulding V,
Merberg D;
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                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system disorders (e.g. stroke) -
                                                                30-MAR-2000; 2000US-0539330.
04-DEC-2000; 2000US-0729674.
                  22-MAR-2001; 2001WO-US09369
                                                                                                                                           (GEMY ) GENETICS INST INC.
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Best Local Similarity
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Treacy M,
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118.265 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98,
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                                                                                                                 August 6, 2002, 16:53:51; Search time 51.22 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-186-811-2
US-08-311-611A-98
US-08-372-783-98
US-08-372-105-98
US-08-306-473A-98
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S-08-209-762-98
S-08-473-344-98
S-08-274-303-6
S-08-377-391A-2
S-08-779-400-2
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US-09-119-263-98
US-08-657-162-98
US-09-224-480-98
US-09-093-539-98
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US-08-431-517F-2
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                                                                                                                                                                                                                                                                                                                                       231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                                                US-10-020-139-2_COPY_2_249
                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                  Perfect score:
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                                                                             OM protein
                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                               Run on:
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Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5245013
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Patent No. 5245013
Sequence 17, Appli
Sequence 9, Appli
Sequence 7, Appli
                              98, Appl
98, Appl
4, Appli
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Appli
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                                            Sequence 98,
Sequence 4, A
Sequence 4, A
Sequence 2, A
Sequence 2, A
                                Sequence
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD. VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/405,496
FILING DATE: 15-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PCT-US94-06931-4
PCT-US94-07844-6
PCT-US95-00498-98
PCT-US95-00498-98
PCT-US95-00566-98
US-08-700-548-4
US-08-785-431-4
US-08-205-048-2
US-08-205-048-2
US-08-205-048-2
US-08-205-048-2
US-08-205-048-2
US-08-206-780-6
US-08-906-780-6
US-08-906-328-2
US-08-990-849-2
                                                                                                                                                                                                                   US-08-431-517F-17
US-08-215-089-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                               US-08-431-517F-7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429 700
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PRIOR APPLICATION DATA:
APPLICATION AND APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/08480604A; Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'AGENT 1ME C. INGOLIA, DIANE E. 40,027
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             ; Patent No. 5736139
; GENERAL INFORMATION:
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101 ----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
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                                                                                                                                                                                                                                                                                                                                                                                5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                   8.5%: Store 104: DB 1: Length 2710;
20.3%: Pred. No. 0.42;
ative 63; Mismatches 109; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NURROTOXIN
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,496A
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220 MONTGOMERY STREET, SULTE 2200
REFERENCE/DOCKET NUMBER: OPHD-01763
TELEOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER (5710 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 MUNICOME
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 56; Conserva
                                                                                                                                                  amino acid
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                                                                                                                                                                                            ; MOLECULE TYP
US-08-480-604A-6
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                                                                                                                                                  TYPE:
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Query Match 8.5%; Score 104; DB 2; Length 2710;
Best Local Similarity 20.3%; Pred. No. 0.42;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRACE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS.
APPLICANT: STAFFORD, DOUGLAS.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
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ADDRESSEE: MEDIEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
APPLICATION NUMBER: US 07/429,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNITED STATES OF AMERICA
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                                                                   NAME: INGOLIA, DIANE E.
REGISTRATION UNDRER: 40.027
REFERENCE/DOCKET UNDRER: 0PHI)-
TELECOMMUNICATION INFORMATION:
TELEFONE: (415, 705-8410
TELEFAX: (415, 39-838
INFORMATION FOR SEQ ID NO: 6: SEQUENCE GRARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acids
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; Patent No. 6290960
                      FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SECUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
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984 STSVKVÖLY---AQLFSTGLNTIYDSIQLVN----LISNAVNDTINVLPTITECI----- 1031
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Best Local Similarity 20.3%; Pred. No. 0.42;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::| |:| :| |:| 867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
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Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
ITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILLIGATION NOWBER: US/09/541,782
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPHD-01763
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAK-1995
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-00T-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPA: (415) 397-8338
INFORMATION FOR SEG ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-915-136-6
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEC ID NO 10
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                                                                                                                                 8.1%; Score 100; DB 4; Length 1057;
24.4%; Pred. No. 0.26;
Live 34; Mismatches 79; Indels 70; Gaps
                                                                                                                                                                                                                                                                        447 LDOCKSDLONKTQELE------TTQKHLQETKLQL-VKBEYITSALESTEEKLH 493
                                                                                                                                                                                                                                                                                                                                                                   494 DAASKLLNTVEE----TTKDVSGLHSKLDRKKAVDQHNAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | : | : | : | 550 KDGSSKQKAMLEVHKTLFGNLLSSSVSALDTITTV-----ALGSLTSIPENV 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 126
                                                                                                                                                                                                                                                                                                                                                                                                               127 ----PVTANVTVAGPIIGQLINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SLSCLDKHSQIINKF------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
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                                                                                                                                                                                                                              21 LDNI.GNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQK--SSAWQLAKQKAQ 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scott, Randal W
APPLICANT: Marra, Marian N
TITLE OF INVENTION: RECOMBINAT ENDOTOXIN-NEUTRALIZING PROTEINS
FILE REPERENCE: 1103/11307US01
CURRENT APPLICATION NUMBER: US/08/431,517F
CURRENT FILING DATE: 1995-05-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%; Score 96; DB 4; Length 481;
19.6%; Pred. No. 0.21;
Live 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 2, Application US/08431517F ; Patent No. 6265187
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                                                                                                                     Query Match
Best Local Similarity 24.48
Watches 59; Conservative
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les 51; Conserva
                      TYPE: PKT
ORGANISM: H.sapiens
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US-08-431-517F-2
LENGTH: 1057
                                                               US-09-541-782-10
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APPLICANT: Fischer et. a). TITLE OF INVENTION: 123 Human Secreted Proteins FILE REFERENCE: P2010P1 CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08 CURRENT APPLICATION NUMBER: US/09/227,357 R FILLING DATE: 1997-07-08
R APPLICATION NUMBER: 60/051,932
R FILING DATE: 1997-07-08
R FILING DATE: 1997-07-08
R FILING DATE: 1997-07-08
R FILING DATE: 1997-07-08 R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/052,795

R FILING DATE: 1997-07-08

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,919

R APPLICATION NUMBER: 60/051,928 EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER LING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER APPLICATION NUMBER: 60/052,803 FILING DATE: 1997-07-08
APPLICATION WUMBER: 60/052,732
ELING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,931 ICATION NUMBER: 60/051,918 FILING DATE: 1997-07-08
APPLICATION UNMBER: 60/051,920
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,733 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/055,722 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,723 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,948 APPLICATION NUMBER: 60/055,949 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,950 FILING DATE: 1997-08-18
APPLICATION UNMBER: 60/055,947
APPLICATION NUMBER: 60/055,947
APPLICATION NUMBER: 60/055,964 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/056,360 FILING DATE: 1997-08-18 APPLICATION UNMBER: 60/055,684 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,984 APPLICATION NUMBER: 60/055,953 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,954 EARLIER APPLICATION NUMBER: 60/058,785 Sequence 195, Application US/09227357 Patent No. 6342581 GENERAL INFORMATION: :: :: |: |: |: 223 DSFADIDYSLVEAPRATAQM 242 FILING DATE: 1997-07-08 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 09-227-357-195 EARLIER / EARLJER | EARLJER / EARLJER / EARLIER g

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105 --NSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 162
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APPLICANT: Carroll, Stephen Filzhugh
APPLICANT: Ma, Jeremy Kam.kuen
APPLICANT: White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 95.5; DB 4; Length 210; 19.2%; Pred. No. 0.069; trive 46; Mismatches 86; Indels 5:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,811
                                                                                                                                                                                                                                                                                                                                                                                         : NAME/KEY: SITE
: LOCATION: (210)
: O'THE INFORMATION: Xaa equals stop translation
US-09-227-357-195
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EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER PILING DATE: 1997-09-12
EARLIER PILING DATE: 1997-09-12
EARLIER PILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER APPLICATION NUMBER: 60/056,661
EARLIER PAPLICATION NUMBER: 60/056,661
SOFTWARE: PALENTING DATE: 1997-09-12
SOFTWARE: PALENTIN Ver: 2.0
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STATE: Illinois
STATE: United States of America
ZIP: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 19.2%
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                    7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cohen, Jonathan
APPLICANT: King, Ada H.:
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Intection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
                                                                                                                                                                                                                                                                                                                    7.7%; Score 94; DB 1; Length 481; 19.6%; Pred. No. 0.33; tive 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/311,611A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98, Application US/08311611A
Patent No. 5523288
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APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ---- NVIQOVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 DSFADIDYSLVEAPRATAOM 242
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                 "rl.BP"
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MEDIUM TYPE: Floppy disk
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                                                                                          : 481 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 19.6%
Matches 51; Conservative
                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                     ) OTHER INFORMATION:
US-08-186-811-2
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Illinois
                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-311-611A-98
                                                                                                                                      TOPOLOGY:
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                                                                                             LENGTH:
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                                                                                                                                                                                     FEATURE
                                                                                                                     TYPE:
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125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
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Patent No. 5578572
GENERAL INFORMATION:
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%; Score 94; DB 1; Length 481;
19.6%; Pred. No. 0.33;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Mismatches 107; Indels
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
                                                       REFERENCE/DOCKET NUMBER: 32251
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                  NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
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INFORMATION FOR SEQ ID NO: 98
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%
Best Local Similarity 19.6%
Matches 51; Conservative
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OTHER INFORMATION: "rLE
US-08-311-611A-98
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                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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STATE:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewis H.
APPLICANT: Scannon, Patrick J.
APPLICANT: Scannon, Patrick J.
ATILLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
                                                                                                                                                                                 NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENDE/DOCKET NUMBER: 27129/32415
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6400
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COUNTRY: United States of America
ZIP: 60606-6402
                 PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/209,762
FILING DATE: 11-XAR-1994
PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/183,222
FILING DATE: 14-1AN-1994
ATTORREY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTEKISTICS:
LENGTH: 481 amino acids
TYPE: amino acid
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; OTHER INFORMATION: "rLBP"
US-08-372-783-98
FILING DATE: 11-JUL-1994
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70 HVGRG-----PGQGLSL 103
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                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Allegretti & Witcoff, Ltd. Suite 3000, 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 98, Application US/08306473A
; Patent No. 5652332
; GENERAL INFORMATION:
PC-DOS/MS-DOS
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/183,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                             Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ----NVIQOVVDNPQHKTQL 244
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OTHER INFORMATION: "rLBP"
                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
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                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPINTDIFGLKISNSLTLDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VLLCGVLTGTSESI,LDNLGNDLSNVVDK-I,EPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
TITLE OF INVENTION: Lipopolysaccharide Binding Protein Derivatives
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.7%; Score 94; DB 1; Length 481;
Best Local Similarity 19.6%; Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107; Indels
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ILBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,473A
                                                                                                                                                                                                                                                                                                                                                                             NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 08/183,222
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; Patent No. 5731415
; GENERAL INFORMATION:
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TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-715-1234
INFORMATION FOR SEQ LD NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                     Illinois
Chicago
                                        USA
                                                                                                                                                                                                                     FILING DATE:
                                                           90909
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                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Protein and Uses Thereof
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.6%; Pred. No. 0.33;
ttive 52; Mismatches 107; Indels 50; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 94; DB 1; Length 481;
19.6%; Pred. No. 0.33;
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                 COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27129/32137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
TORNEY AGENT.
                                                                                Illinois
United States of America
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                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 45.
TOTAL STATE INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879.
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
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OTHER INFORMATION: "rLBP"
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LENGTH: 481 amino acids
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GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
TITLE OF INVENTION: Method For Potentiating BPI Protein Bactericidal
TITLE OF INVENTION: Activity By Administration Of LBP Proteins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 SFPVTANVTVAG--PIIGQIINLKASLDL-L.TAVT1ETD-----PQTHQPVAVLGECASD 176
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Best Local Similarity 19.6%; Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107; Indels 50; Gaps
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/473,344 FILING DATE: 7-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/306,473 FILING DATE: 15-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             PC-DOS/MS-DOS
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; Patent No. 5770561
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-715-1234
TELEFAX: 910-221-5337
INPERMATION FOR SEO ID 00: 98:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 481 amino acids
amino acid
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STATE: Illinois
                           90909
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COUNTRY:
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TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Enctional Domains of Bactericidal/Permeability-Increasing
TITLE OF INVENTION: Protein and Uses Thereof
NUMBER OF SEQUENCES: 96
CORRESPONDENCE BORNESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.7%; Score 94; DB 1; Length 481;
Best Local Similarity 19.6%; Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SIS-DSSIRVOGRWKVRKSFFKLOGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
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                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,762
FILING DATE: 11-JAN-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: No. 5733872nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Application US/08473344 Patent No. 5763567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312-715-1234
TELEEX: 910-221-5317
INFORMATION FOR ESO 10 00: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ----NVIQQVVDNPQHKTQL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: "rLBP"
US-08-209-762-98
                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 amino acids
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                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
Chicago
: Illinois
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STATE: Illinois
                                                            USA
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                                                            COUNTRY:
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                              STATE:
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Ouery Match 7.7%: Score 94; DB 1; Length 481;
Best Local Similarity 19.6%; Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SIS-DSSIRVOCHWKVRKSFFKLOGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 PTSISLSLLDKHSQ11NKFVNSVIN----TLKSTVSSILQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 IADVEVDMSGDLGWLLNLFHNQTESKFQKVLESRTCEMIQKSVSSDLQPYLQTTET 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 QKSSAWQLAKQKAQEAEKLLNNVISKLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VLLCGVLTGTSESILDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTL NE Release #1.0, Version #1.25
CURRNY APPLICATION DATA:
APPLICATION NUMBER: US/08/274,303
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Sharp Jeffrey S.
REGISTRATION NUMBER: 31.879
REFERENCE/DOCKET NUMBER: 32157
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 312/474-6408
INFORMATION FOR SEQ. ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: allocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 ----NVIQQVVIJNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 DSFADIDYSLVEAPRATAGM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; OTHER INFORMATION: "rLBP"
US-08-274-303-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
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Search completed: August 6, 2002, 16:53:52 Job time: 284 sec

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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: August 6, 2002, 17:05:12; Search time 66.51 Seconds (without alignments) 310.618 Million cell updates/sec

310.618 US-10-020-139-2\_COPY\_35\_249 Sequence: 1 KLEPVLHEGLETVDNTLKGI......NVIQQVVDNPQHKTQLGTLJ 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Perfect score:

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIK\_71:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		G				
Result		Query				
No.	Score	Match	Length	DB	QI	Description
7	294.5	۲.	235	Ч	SOMS	parotid secretory
2	263.5	24.8	235	7	B42337	secre
6	154.5	4	206	7	A42337	•-
4	106		296	~	A49943	fructose-bisphosph
ഹ	106		1769	7	S53378	۵
9	103.5	9.6	296	7	F90067	
7	99.5	٠.	1727	7	T50073	U
80	98.5	9.3	1615	٦	WMTM8T	
6	97.5		211	7	D64505	1 p
10	96.5	9.1	1345	7	H90975	hypothetical prote
11	96.5	9.1	2660	7	E85822	probable invasin Z
12	95		619	7	D64182	DNA ligase (NAD+)
13	95		1130	7	T19148	hypothetical prote
14	94.5		825	7	B89944	
15	94.5		1729	7	S57596	⋖
16	93.5		1038	~	S37854	hypothetical prote
17	93.5	æ	2938	7	T30249	cell proliferation
18	93		624	7	PC6003	surface membrane p
19	66		1237	7	AC1583	internalin protein
20	92.2	8.7	414	7	T27045	hypothetical prote
21	92.5	8.7	928	7	S64249	_
22	92		2383	7	D64962	probable membrane
23	91.5		473	7	S17448	probable ligand-bi
24	91	8.0	443	7	B82209	GGDEF family prote
25	91	•	454	~	T18765	hypothetical prote
26	91	•	578	~	B82204	methyl-accepting c
27	91	٠.	7	~	3705	toxin A - Clostrid
58	90.5	B.	1254	7	E82064	conserved hypothet
29	90.5	8.5	ð	~	6027	IgA-specific metal

0	0	or or	500	-	OS ANDA	1 000	cell fusion alvoor
	ים מ	0 00	1056		602157	inonia	kinesin-like snind
3.5	1 . O &	. 4	2819	4 (	A90551	Conser	conserved hypothet
33	00	4.	368	N	A11254	probab	probable peptidogl
34	60	8	481	N	156246	lipopo	lipopolysaccharide
35	68	8.4	1075	7	T52638	export	exportin 1 (valida
36	68	8.4	1075	(7)	T51557	Export	Exportinl (XPO1) p
37	88.5	80 .3	1509	C)	B89985	hypoth	hypothetical prote
38	87.5	8.2	602	2	E71562	hypoth	hypothetical prote
39	87.5	8.2	707	N	T29559	hypoth	
40	87.5	8.2	066	C)	C82759	zinc p	zinc proteinase XF
4.1	87.5	8.2	6713	N	B89921	hypoth	hypothetical prote
42	87	8.2	310	?	F90011	conser	conserved hypothet
	8.7	8.2	621	~	T15859	hypoth	hypothetical prote
44	9	8.2	256	N	877810	probab	probable DNA topoi
4.5	86.5	8.2	899	2	139902	penici	penicillin-binding
					ALIGN	ALIGNMENTS	
							•
RESULT	7						
SOMS							
parotid secretory protein precursor	secretor	y prote	in pre	cur	sor - mouse	lse .	
N:Alternate names: PSP	ate name	S: PSP					
C; Species: Mus musculus (house mouse)	S: Mus m	nscnjns	(hous	e E	onse)		
C;Date: 31-Dec-1988 #sequence_revision	31-Dec-1	988 #se	adneuce	re	vision 31	31-Dec-1988 #text_change 2	22-Jun-1999
C;Access	ion: A23	031; IS	3236				
R; Madsen, H.O.; Hick	, H.O.:	, ( tH	J.P.				
Nuclot	, i		1-13, 1985	198	5		
.:		•	ing of	5	ing of mouse PSP mRNA.	IRNA.	
			u 'TCO	7	00+01700:		

3 3 2

.01697; NID:953810; PIDN:CAA25846.1; PID:9758163
B.K.; Mikkelsen, B.M.; Harmark, K.; Nielsen, J.T.; Hjorth, A.

Murine parotid secretory protein and salivary amylase expr.

anslated from GB/EMBL/DDBJ

C. Comment: PSP is the most abundant protein in the parotid gland. Its function is not comment: PSP is the most abundant protein in the parotid gland. Its function is not comment: PSP is the most abundant protein in the parotid gland. Its function is A; Gene: PSP A; Map Position: 2
A; Nate position: 2
A; Introns: 4//1
A; Note: list of introns may be incomplete
C; Superfamily: parotid secretory protein
C; Reywords: parotid gland; saliva
C; Reywords: parotid gland; saliva
F; 1-20; Domain: signal sequence #status predicted <SIG>F; 1-235/Product: parotid secretory protein #status predicted <MAT>

Query Match
27.8%; Score 294.5; DB 1; Length 235;
Best Local Similarity 32.7%; Pred. No. 2.8e-16;
Matches 69; Conservative 55; Mismatches 74; Indels 13; Gaps

OY 114 ASLDLLTAVTTETDPOTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKST 173

Db 135 VSLDLINSLSIKTNAQTGLPEVTIGKCSSNTDKISILGRRLPIINSILDGVSTLLTST 194

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fructose-bisphosphate aldolase (EC 4.1.2.13) - Staphylococcus carnosus (strain TM300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Cloning, sequencing, and characterization of the gene encoding the class I A;Reference number: A49943; MUID:94042930 A;Accession: A49943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, February 1995
A;DescriptLibrary, A;DescriptLibrary, MEF2, GSH1
A;Reference number: S53376
A;Reference number: S53378
A;Reference number: S53378
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Staphylococcus carnosus
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 15-Oct-1999
C;Accession: A49943; S33358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: LNA
A;Residues: 1-296 <WIT>
A;Cross-references: EMBL:X71729; NID:g297873; PIDN:CAA50663.1; PID:g297874
C;Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 NNKEAIE--KVVKQQFEVAKEIIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ----LLTAVTIET-----DPQTHQPVAVLGECASDPTSI: LSLLDKHSQ1INKF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LKIKDLRILNLNHEVSPNGDEVTLKMPMALNASLSLPARDLTTDVSISMEAITSFAIEKD 125
                                                                              128 POTHOPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:249384; NID:91008292; PID:91008293; MIPS:YJL109c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YJL109c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.0%; Score 106; DB 2; Length 296 Best Local Similarity 25.9%; Pred. No. 0.43; Matches 50; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Rasmussen, S.W. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1769 <RAS>
A;Cross-references: EMBL:X85021; NID:9728698; PID:9728701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N:Alternate names: hypothetical protein J0808
C:Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R,Wilke, C.; Goetz, F.
J. Bacteriol. 175, 7495-7499, 1993
                                                                                                                                                                                              188 JFIHSLDVNVIQQVVDNPQ 206
                                                                                                                                                                                                                                                     186 I, IISN --- TFHPDEISNPQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 VNSVINTLKSTVS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 SRALVSDLNAQQS 273
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A; Residues: 1-1769 <RAW>
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J. Biol. Chem. 267, 2679-2687, 1992
J. Biol. Chem. 267, 2679-2687, 1992
A.Filtle: Noonatal rat Submandibular gland protein SMG-A and parotid secretory protein an A;Reference number: A42337; MUID:92129360
A.Accession: B42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Mirels, L.; Ball, W.D.
J. Biol. Chem. 267, 2679-2687, 1992
A.Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein ar
A;Reference number: A42337; MUID:92129360
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                                                                                                                                                                                                                         N.Alternate names: PSP
C.Species: Rattus norvegicus (Norway rat)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Auy-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway ral)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 TDPQTHQPVAVI,GECASDPTSISLSLLDKHSQJINKFVNSVINTLKSTVSSLLQKEICPL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 LKISNSLILLDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 --LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 LLLRVNKFRVLDLQAGLSSNGKDIDLKLPLVFEISFSLPVIGPTLDVAVSLDLLNSVSVQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG 67
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A.Note: sequence extracted from NCBI backbone (NCBIN:78707, NCBIP:78708)
C.Superfamily: parotid secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-255 cMIX-
A;Coss-references: GB:M83209; NID:g206456; PIDN:AAC06334.1; PID:g206457
A;Note: sequence extracted from NCBI backbone (NCBIN:78709, NCBIP:78710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.8%; Score 263.5; DB 2; 29.6%; Pred. No. 8.3e-14; tive 56; Mismatches 75;
                              :|::|| :|||: : :|: :| :: |
195 LSTVLQNFLCPLIQYVLSTLNPSVLQGLLSN 225
174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                 parotid secretory protein precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: parotid secretory protein C;Keywords: parotid gland; saliva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submandibular gland protein A - rat
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Matcher 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 59; Conserv
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A; Residues: 1-206 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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Gaps

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A:Molecule type: genomic RNA
A;Residues: 1-1615 COHN>
A;Note: readthrough of the terminator UAG between codons for Gln-1116 and Gln-1117 c
C;Superfamily: cucumber mosaic virus RNA 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1727 <MCD>
A;Cross-references: EMBL:AL133357; PIDN:CAB62414.1; GSPDB:GN00066; SPDB:SPAC1486.04<
A;Experimental source: strain 972h(-); cosmid c1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Ohno, T.; Aoyagi, M.; Yamanashi, Y.; Saito, H.; Ikawa, S.; Meshi, T.; Okada, Y. J. Balochen. 96, 1915-1923, 1984
A;Title: Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and A;Reference number: A91984; MUID:85157522
                                                                                                                                                                                                                                                                   myosin-like coiled-coil protein sp8 [imported] - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                            C; Species: Schizosaccharomyces pombe
C; Date: 09-Jun-2000 sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C; Accession: T50073
R; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. submitted to the EMBL Data Library, December 1999
A; Reference number: 225034
A; Reference number: 225034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 VKAEFIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 VQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSRNVPATVQ--VA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 LGECASOPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSL--D 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 LDEYAQNPSTASETLVNK -- ELAN -----FSSIKEAVSKTLE -----LREKVRALECD 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
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20.4%; Pred. No. 16;
Live 44; Mismatches 79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 KLKVDLGVLQKSSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 99.5; DB 2; Length 1727; Best Local Similarity 26.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180K protein - tomato mosaic virus (strain L)
N;Contains: 130K protein
C;Species: tomato mosaic virus
                            150 --SLLDKHSQIINKFVNSVINTLKSTVS 175
                                                                                             246 ANELLKDNDELIASFSRALASDLRADQS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Conservative
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Best Local Similarity
Matches 40; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 VNV100VV 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Lancet 357, 1225-1240,,2001
R;Rasmussen, S W. Yeast 11, 673-883, 1995
A;Title: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3
A;Reference number: S57357; MUID:96090136
A;Accession: S57359
                                                                                                                                                                                                                        A.Residues: 1-1769 - RAF>
A.Cross-references: EMBL:X85021; NID:9728698; PIDN:CAA59385.1; PID:9728701
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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A;Cross-references: GB:BA000018; PID:g13702563; PIDN:BAB43704.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SA2399 (imported) - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Staphylococcus aureus
C;Date: 10-May-2001 *sequence_revision 10-May-2001 *text_change 22-Oct-2001
C;Accession: F90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 KLNIILSLLKK-----IRLERYEVRLIITOLIYLSEILEDKSQLVELFEYFISINEDLV 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 V----ETTKKUTASFQTFLDKHSELINTTNVSMLTETGERYKKVLSLFTEAIGKGYKASS 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 LKCL-----KSLGLT-----GELFEIRLTTSLFTNADVNTDIVKQLSDP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 VAVLGECASDPTSISLSLLDKHSQIIN-----K 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ----LKASLDLLTA-----VTIETDPQTHQPVAVLGECASDPTSISL------ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 106; DB 2; Length 1769;
; Pred. No. 4.5;
44; Mismatches 73; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 EGKYTADYLADKGVVPFLKVDKGLAEEQNGVQLMKP-----IDNLDSLLDRANERHI 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNV1--SKLLPTNTD1-----FGLKISNSLI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLOVNVIQOVVDNPQHKTQLQTL1 215
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19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: transmembrane protein
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A.Experimental source: strain O157:H7, substrain RIMD 0509952 C.Genetics: A:Gene: ECs2776	Query Match Best Local Similarity 23.4%; Pred. No. 18; Matches 54; Conservative 36; Mismatches 70; Indels 71; Gaps 11; QY 50 LLNVISKLIPPITDI-FGIRISNSLILDV-KAE	Qy 87 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120	RESULT 11 E85822 probable invasin 23135 [imported] - Escherichia coli (strain O157:H7, substrain EDL93: C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E85822 R;Perna, N.T.: Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apode Nature 409, 529-533, 2001	A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A:Reference number: A85480; MUID:21074935; PMID:11206551 A:Accession: E85822 A:Status: preliminary A:Molecule type: DMA A:Residues: 1-2660 <sto> A:Cross-references: GB:AE005174; NID:912516151; PIDN:AAG57041.1; GSPDB:GN00145; UMGP:A:Escherimental source: strain 0157:H7. substrain EDL933 A:Gene: Z3135</sto>	Ouery Match Best Locat Similarity 23.4%; Pred. No. 44; Best Locat Similarity 23.4%; Pred. No. 44; Matches 54; Conservative 36; Mismatches 70; Indels 71; Gaps 11; Cy 50 ILNNVISKLPTNTDI-FGLKISNSILILOV-KAE	Db 1955 KQVTLIADAGTAKLASLTSVYSFVVSTTEGATMT QY 121 AVTIETDPQTHQPVANLGECASDPTSISLSLLDK S : :    :
QY 83 IDDGKGLNLSFPVTANVTVAGPIGQIINLKASLDLLTAVTIETDPQT 130 :	OY 131 HOPVAVLGECASUPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLOKEICPLIRI 188 :  ::   ::   ::   ::   ::   ::   ::	RESULT 9 D64505 hypothetical protein MJ1646 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Mathanococcus jannaschii C;Date: 13.Sep-1996 #sequence_revision 13.Sep-1996 #text_change 29.Sep-1999 C;Accession: D64505 R;Bult, C.J.: White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.: Worbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; ArTitle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii	A;Accession: D64505 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-211 <bui.> A;Cross-references: GB:U67605; GB:L77117; NID:g1592227; PIDN:AAB99667.1; PID:g1500547; TC;Genetics: A;Map position: FOR1628443-1629078 C;Superfamily: conserved hypothetical protein MJ1646</bui.>	Ouery Match  9.2%; Score 97.5; DB 2; Length 211;  Best Local Similarity 24.0%; Pred. No. 1.3;  Matches 56; Conservative 35; Mismatches 75; Indels 67; Gaps 11;  Oy 5 VLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAOEAEKLLNNVISKLI.PTN 62	112	Arbour 10  RESOLT 10  RESOLT 10  RESOLT 10  RESOLT 10  RESOLT 10  Rypothetical protein ECs2776 [imported] - Escherichia coli (strain 0157:H7, substrain RI C: Species: Escherichia coli C: Species: Escherichia coli C: Stacession: H90975  R: Hayashi, T.: Makino, K.; Ohnishi, M.: Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  DNA Res. 8, 11-22, 2001  A: Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A; Recession: H90975  A: Reference number: A99629; MUID:21156231; PMID:11258796  A; Status: preliminary A; Residues: 1-145 < HAY> A; Residues: 1-145 < HAY> A; Residues: 1-145 < HAY> A; Cross-references: GB:BA000007; PIDN:BAB36199.1; PID:g13362244; GSPDB:GN00154

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C;Accession: B89944
R;Kuroda, M: Ohta, T: Uchiyama, I:; Baba, T:; Yuzawa, H:; Kobayashi, I:; Cui, L:; ma, A: Mizutani-Ui, Y:; Kobayashi, N.; Sawano, T:; Inoue, R:; Kaito, C:; Sekimizu, C:; Shiba, T:; Hattori, M:; Ogasawara, N:; Hayashi, H:; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-825 <KUR>
A;Cross-references: GB:BA000018; PID:g13701417; PIDN:BAB42711.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89944
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SA1447 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                        76 ------LDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 129
                                                                                                                                                                                                                                                                                                                                                766 SLEFFDFQLETTPIMDAKQHNMDFTTVYDVLVSNLLIHYL------- 806
                                                                                                                                                                                                                                                                                                                                                                                                               130 THQPVAVLGECASD-----PTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 K------AQEAEKLLNNVISKLLPT---NTD----IFGLKISNSLI----- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 NS------LILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 KASLDLLTAVTIETD----PQTHQPVAVLGECA-----SDPTSISLSLLDKHSQIINKF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 KAAL----LYTLEEECIKOGHTYLPINVVIDLTVDVLNYQDEEVIEPEKLDEMLOYLNEE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 VNSVINTLKSTVSSLLQKEICP---LIRIFIHSLDVNVIQQ-----VVDNPQ---- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 KRLIIDNEQVAIPSLYYSEIKSVQNLFRIKTHTNKLTEIEQSDLQMHIGEIEDANQVNYA 340
                                                  1 KLEPVLHEGLETVDN-----TLKGILEKLK-VDLGVLQKSSAWQLAKQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Mismatches 87; Indels 67; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal RNA processing protein RRP5 - yeast (Saccharomyces cerevisiae)
N;Alternate names::protein YM9959.11c; protein YMR229c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.5%; Pred, No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 PLIRIFIHSLDVNVIQOVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 TL-----RYELEVSOPISDS 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 ASOKEALOTAI 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SA1447
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A.Introns: 35/2; 72/1; 119/2; 141/3; 183/2; 225/2; 325/2; 369/3; 492/2; 579/2; 645/3; 67
C;Accession: D64182
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                     A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630 A;Accession: D64182
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U32789; GB:L42023; NID:91574642; PIDN:AAC22753.1; PID:91574651; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C09G5.8 - Caenorhabditis elegans
C;Species: T19148; T20147
R;Palmer, S.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z19080
A;Accession: T19148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1130 <WIL>
A;Residues: 1-1130 <WIL>
A;Residues: Dealminary; translated from GB/EMBL/DDBJ
A;Reference number: Z1929
A;Accession: T20147
A;Reference number: Z1929
A;Accession: T20147
A;Residues: 1-1130 <WIZ>
A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-1130 <WIZ>
A;Cross-references: EMBL:Z46792; PIDN:CAA86767.1; GSPDB:GN00020; CESP:C09G5.8
A;Reperimental source: clone C52A11
C;Genetics:
A;Genetics:
A;Genetics:
A;App nocition: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 EP--VFVAGVTVSNATLHNG----- DEIERLNIAIGDTVVIRRAGDVIPQII------ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 -- GVLHERRPDNAKPIIF-----PTNCPVC----DSQIIRIEGEAVARCTGGLFCAAQ 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VDNTLKGILE-KLKVDLGVLQKSSAWQLA-KQKAQEAEKLLNNV------ISKL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown; translation not shown
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9.0%; Score 95; DB 2; Length 1130;
Best Local Similarity 24.9%; Pred. No. 19;
Matches 65; Conservative 33; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 95; DB 2; Length 679; 24.5%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Pred. No. 9.0;
ttive 40; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     A)Start codon: GTG
C;Superfamily: polydeoxyribonucleotide synthase (NAD+)
C;Keywords: DNA repair; DNA replication; ligase; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 QKEICPLIRIFI--HSLDVN-----VIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 RKE---ALKHFVSRKAMDIDGVGGKLIEOLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Conservative
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-679 <TIGR>
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C; Species: Saccharomyces cerevisiae
C; Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C; Accession: 557596; $72446
S; Skelton, J.; Churcher, C.M.
Submitted to the EMBL Data Library, June 1995
A; Accession: 557596
A; Accession: 557596
A; Accession: 557596
A; Reference number: S57587
A; Reference number: S7587
A; Reference number: S7587
A; Reference number: S72446; MUD: 9887599; PIDN: CAA90200.1; PID: 9887610; MIPS: YMR2296
A; Experimental source: EMBL: 249939; NID: 9887599; PIDN: CAA90200.1; PID: 9887610; MIPS: YMR2296
A; Reference number: S72446; MUD: 97051828
A; References: EMBL: 249939; NID: 9887599; PIDN: CAA90200.1; PID: 9887610
A; Cross-references: EMBL: 249939; NID: 9887599; PIDN: CAA90200.1; PID: 9887610
A; Genetics
C; Genetics
C; Function:
A; Description: required for pre-rMNA processing
C; Superfamily: ribosomal RNA processing
C; Superfamily: ribosomal RNA binding
C; Superfamily: ribosomal RNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 -----VTVAGPIIGQIINLKA----SLDL-------LTAVTIETD------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 SDKGLEVAFNGKFIGLVLPSYAVDSRDIDJSKAFY INOSVTVYJ.LKTDDKNQKFILJSIJKA 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ETVDNTLKG------ILEKI.K------VDI.GVLQKSSAWQI.AKQ--KAQE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 AEKLLNNVISKII.PTNTDIFGLKISNSLILDVKAEPI --- - DDGKGLNI,SFPVTAN ---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 6, 2002, 17:05:14 Job time: 916 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916 ANLHGRVDIAEVFDTYEEITDKKQ 939
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August 6, 2002, 17:07:32 ; Search time 32.88 Seconds (without alignments) 253.184 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q10339 schizosacch P33420 saccharomyc P46674 saccharomyc P40108 cladosporiu P70782 agrobacteri P16328 salmonella P54861 saccharomyc Q97583 methanococc Q07585 bacillus su P30436 oncorhynchu P05214 mus musculu				Craniata; Vertebrata; Euteleostomi: Sciurognathi; Muridae; Murinae; Mus.
YBM2_SCHPO N180_YEAST SAC3_YEAST DHAL_CLAHE EFG_AGRTU FFLID_SALTY DNMI_YEAST BP28_HUMAN Y432_METJA YHDP_BACSU TBA_ONCKE TBA3_MOUSE	ALIGNMENTS	PRT; 235 AA.	010/43; 100/43; 01-AUG-1988 (Rel. 08, Last sequence update) 01-AUG-1997 (Rel. 35, Last annotation update) parotid secretory protein precursor (PSP).	
7.9 615 1 7.9 868 1 7.8 496 1 7.8 496 1 7.8 469 1 7.8 757 1 7.7 366 1 7.7 444 1 7.7 444 1		STANDARD;	(Rel. 08, Created) (Rel. 08, Last seq (Rel. 35, Last ann etory protein prec	(Mouse). etazoa; Chordata; theria; Rodentia; 0090;
3.4 9.3 9.3 9.3 9.3 9.3 9.3 9.3 9.3	 E.	PSP_MOUSE ID PSP_MOUSE	PU//43; 01-AUG-1988 01-AUG-1988 01-NOV-1997 Parotid secr	Mus musculus (Mouse) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
<u> </u> ж м м м м м м м м м м м м м м м м м м	E-1110	PSP	AC DE CONTRACTOR CONTR	8008 8008

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PAROTID SECRETORY PROTEIN.
23311BAE1E6E2EF3 CRC64; EMBL; M26807; AAA40009.1; ... EMBL; M26806; AAA40009.1; JOINED. 24753 MW; EMBL; X01697; CAA25846.1; -. 20 PIR; A23031; SQMS. MGD; MGI:97787; Psp. Parotid gland; Signal SIGNAL 1 20 235 AA; SEQUENCE 

Gaps

27.8%; Score 294.5; DB 1; Length 235; 32.7%; Pred. No. 6.5e-17; Live 55; Mismatches 74; Indels 13;

Query Match 27.8% Best Local Similarity 32.7% Matches 69; Conservative

amylase expression.";
EMBO J. 5:1891-1896(1986).
-!- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.
-!- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTION IS COORDINATED
WITH THAT OF SALIVARY AMYLASE.

MEDLINE-87004556; PubMed-2428613; Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harmark K., Nielsen J.T., Hjorth J.P.; Nielsen J.T., Hjorth J.P.; "Coordination of murine parotid secretory protein and salivary

SEQUENCE OF 1-87 FROM N.A. STRAIN-C3H; TISSUE-Spleen;

TISSUE-Parotid gland;
MEDLINE-85215456; PubMed=2582349;
Madsen H.O., Hjorth J.P.;
Molecular cloning of mouse PSP MRNA.";
Nucleic Acids Res. 13:1-13(1985).

SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ICR: TISSUE-Palate;
MEDLINE-9240770; PubMed-10024143;
MEDLINE-9240770; PubMed-10024143;
MEDLINE-9240770; PubMed-10024143;
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
"Differential display identification of plunc, a novel gene expressed in embryonic palate, nasal epithelium, and adult lung.";
J. Biol. Chem. 274:13698-13703(1999).
                                                                                                                                                           114 ASLDLLTAVTIETUPQTHQPVAVLGECASDPTSISLSLLDKHSQLINKFVNSVINTLKST 173
                                                                                                                                                                                  56 SKLLPTNTDIFG--LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLK 113
                                                                                                                  75 LGNLKSFTSLNGLLLKINNLKVLUFQAKLSSNGNGIDLTVPLAGFASLVLPFIGKTVDIS 134
                                    19 ESLIGE-IGSAVNNLKII.NPPSEAVPONLNLDVEILOOATSWPLAKNSILET---LNTAD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeClair E.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.;
"Genomic organization of the mouse plunc gene and expression in the
3 EPVLHEGLETVDNTLK-----GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weston W.M., LeClair E.E., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
J. Blol. Chem. 275:8262-8262(2000).
J. Blol. Chem. 275:8262-8262(2000).
I. FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor progression (By similarity).
-:- SUBCELLULAR LOCATION: Secreted (By similarity).
-:- SUBCELLULAR LOCATION: Secreted (By similarity).
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-MAR-2002 (Rel. 41, Last ammotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 284:792-797(2001).
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                                                                                                                                                                                                                                                                      195 LSTVLQNFLCPLLQYVLSTLNPSVLQGLLSN 225
                                                                                                                                                                                                                                               174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                         PKT;
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MGD; MGI:1338036; Plunc.
Signal; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                      PLUN_MOUSE
P97361;
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143 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
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                                                                                                                                                                                                                                                                                                                                  207 SPGSLKISLLNGVTP-VQSFVDNLTGILTKVLPELIQGKVCPLVNGILSGLDVTLVHNIA 265
                                                                                                                                                                                                                                                                                 90 LGILENIPLLDVIKSGGGNSNGI,VGGLLGKLTSSVPLLNNILDIKITDPQLLELGLVQSP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein) (Lung specific X protein) (Nasopharyngeal carcinoma-related protein) (Tracheal epithelium enriched protein).
                                                                                                                                                                                                                                                28 I.GVLQKSSAWQLAKQKAQEAEKI.I.NNVISKL---LPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iwao K., Watanabe T., Fujiwara Y., Takami K., Kodama K.,
Higashiyama M., Yokouchi H., Ozaki K., Monden M., Tanigami A.;
"Isolation of a novel human lung-specific gene, LUNX, a potential
molecular marker for detection of micrometastasis in non-small-cell
        PROTEIN PLUNC.
4 X 6 AA REPEATS OF G-[LPQ]-[PL]-L-P-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the human plunc gene, a gene product with an upper airways and nasopharyngeal restricted expression pattern."; Blochim. Biophys. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3] SEQUENCE FROM N.A. He Z.W. Yao K., Xie L., Zhang L., Fe Z.W., Yao K.T., Xu L.G., Ren C.P., Lan K., Xie L., Zhang L., Liu W.D., Zhou W., Wang L.; "Cloning a new gene related to nasopharyngeal carcinoma."; "Cloning a new gene related to RMBL/GenBank/DDBJ databases.
                                                                                                      N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
7F40BED9859188FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NP55: Q9NZTO:
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein Plunc precursor (Palate lung and nasal epithellum clone
                                                                                                                                                                                    DB 1; Length 278;
                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                        17.5%; Score 185.5; DB 25.0%; Pred. No. 5e-08; tive 44; Mismatches E
PO'LENTIAL.
                                                             REPEAT 2.
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                                            REPEAT
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MEDLINE-21150203; PubMed-11251963;
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Bingle C.D., Bingle L.;
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                                                                                                                                          28611 MW;
                                                                                                                                                                                                                        47; Conservative
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Beridgeman A.M., Brown A.J.,
RA Ghapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Graham D.V., Griffills G.J., Deadman R., Dhami P., Dunn M.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Krights A., Laird G.K., Lavlor S.,
RA Marsh V.L., Martin S.L., Acconachle L.J., McLay M., Connor M.J., McLay M., McConnachle L.J., McLay W., McLay K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showhken R., Sins S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.,
RA Roder S.J.,
RA Roder S.J.,
RA Roder S.J.,
RA Roder S.J.,
RA Miniang L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21317946; PubMed-11425234;
Lindahl M., Stahlbom B., Tagasson C.;
Lindahl M., Stahlbom B., Tagasson C.;
"Identification of a new potential airway irritation marker, palate
lung nasal epithelial clone protein, in human nasal lavage fluid with
two-dimensional electrophoresis and matrix-assisted laser
description/ionization-time of flight.";
Electrophoresis 22:1795-1800(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Upper airways and nasopharyngeal regions, including trachea and nasal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN PLUNC.
Q -> K (IN REF. 1; AAF70860).
EDF152FBC35315BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Gaps

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16.8%; Score 178; DB 1; Length 256; 24.5%; Pred. No. 1.8e-07; tive 44; Mismatches 92; Indels

Conservative

Best\_Local Similarity Matches 46; Conserva

Query Match

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                                                                                                                                                                       144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                                            184 PGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPELVQGNVCPLVNEVLRGLDITLVHDIV 243
                                                85 DCKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0c1-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-ructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Witke C., Goetz F.; "Cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHIFF-BASE WITH DIHYDROXYACETONE-P (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; $33358; $33358.

PIR; $49943; $49943.

PIRSP: P14223; JACC.

InterPro; IPR000741; Aldolase_I.

Pfam; PF00224; $41ycolyttc_enzy; 1.

Propom: P001128; Aldolase_I; 1.

PROSITE: PS00158; ALDOLASE_CLASS_I; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDL,INE=94042930; PubMed*8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol, 175:7495-7499(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyase, Schiff base, Glycolysis.
INIT_MET 0 0 0 BINDING 211 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kula M.R., Brockamp H.P.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus carnosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 NMLIHGLQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID*1281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-TM300
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007159:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 V----ETTKKDTASFQTFLDKHSELINTINVSMLTETGERYKKVLSLFTEAIGKGYKASS 510
362 KLNIILSLLKK-----IRLERYEVRLIITDLIYLSEILEDKSQLVELFEYFISINEDLV 415
                                             76 I.DVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD--PQTHQP 133
                                                                                        416 LKCL-----KSLGLT------KSLGLT------GELFEJRLTTSLFTNADVNTDIVKQLSDP 454
                                                                                                                                 134 VAVI,GECASDPTSISLSLLLDKHSQIIN------K 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jimenez M., Petit T., Gancedo C., Goday C.;
"The alml+ gene from Schlzosaccharomyces pombe encodes a coiled-coil
"The alml+ gene from Schlzosaccharomyces pombe encodes a coiled-coil
protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,
CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                           162 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                      "Generation and analysis of GFP-gene fusion library of fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLED COIL (POTENTIAL).
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COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                    ALMI_SCHPO STANDARD; PKT; 1727 AA 09UTK5; 013313; 09UTR8; 16-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abnormal long morphology protein 1 (Sp8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL133357; CAB62414.1; -.
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20123449; PubMed=10660053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443
542
804
1223
1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-968 H90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coiled coil
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                                                                                                                                                                                       93 KGIVPFLKVDKGLAEEADGVQLMK-P1PDLDKLLDRA-----NERGIFGTKM-RSNILE 144
                                                                                                                                                                                                                                                   78 VKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIIN--------LKASLD-- 117
                                                                                                                                                                                                                                                                                              145 NNKEAIE--KVVKQQFEVAKEIJAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 202
                                                                                                                                                                                                                                                                                                                                            118 -----LLTAVTIET-------DPQTHQPVAVLGECASDPTSISLSLDKHSQIINKF 162
                                                                                                                                                                                                                                                                                                                                                                               203 KKDQYVMLKLTIPTKVNAYSELIEHPQVIRVVALSGGYSRDEAN---KILKQNDGLIASF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLI 75
                                                                                                                     48; Gabs
                                                                                                                                                             18 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLI,NNVISKLLPTNTD1FGI,KISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSI and CSD3 genes, a TCP-1 related gene, an open reading frame similar to the DAL80 gene, and a tRNA(Arg)."; yeast 11:873-883(1995).

--- SIMILARITY: BELONGS TO THE BAP28 FAMILY.

--- SIMILARITY: CONTAINS 1 HEAT REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
200.0 kDa protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 106; DB 1; Length 1769; 19.2%; Pred. No. 1.4;
                                                                     10.0%; Score 106; DB 1; Length 295; 25.9%; Pred, No. 0.14; tive 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            064480D1D249B241 CRC64;
       295 AA; 32720 MW; A189E75574F1FCC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>::</del> ::
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tive 44; Mismatches
                                                                                                                  Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C / FY1679;
MEDLINE-96090136; PubMed-7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAT
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InterPro; IPR000357; HEAT_repeat.
PROSITE; PS50077; HEAT_REPEAT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 SRALVSDLNAUQS 272
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REPEAT 1729 17
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                                                                                               Best Local Similarity
Matches 50; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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P42945;
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           SEQUENCE
                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRPO_TOMK2 STANDARD; PRT; 1616 AA.
P89675; p90349;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
17-007-2001 (Rel. 40, Last annotation update)
18-007-2001 (Rel. 40, Last annotation update)
19-007-2001 (Rel. 40, Last annotat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                  404 KLOLDRLTNKFSSFCEQVKORIPVVKQORSEIVRNNIYMNFLSES-----LETSNNNLTK 458
                                                                                                                                                                                                                                                                                                                                                                      78 VKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQ/INLKASLDLLTAVTIETDPQTHQPVAV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                       459 VQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSRNVPATVQ--VA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 LGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSL--D 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 LDEYAQNPSTASETLVNK--ELAN-----FSSIKEAVSKTLE-----LREKVRALECD 562
                                                                                                                                                                                                                                     23 KLKVDLGVLQKSSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Biol. (Mosk) 31:826-830(1997).
FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAPTING AND AND AND HELD THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001788; RNA_dep_RNApol2.
Interpro; IPR001288; V_methyltransf.
Interpro; IPR000606; Viral_helicasel.
Pfam: PF00478; RNA_dep_RNApol2; 1.
Pfam: PF01448; Viral_helicasel: 1.
Pfam: PF014660; Vmethyltransf; 1.
Transferase; RNA-directed RNA_polymerase; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K.; *Properties and structure of the tobacco mosaic virus strain \rm K2
                                                                                             9.4%; Score 99.5; DB 1; Length 1727; 26.1%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
W; C2F5CE0C8C965336 CRC64;
                                                                                                                                                                     74; Indels
197858 MW; F820BF8D9C132644 CRC64;
                                                                                                                                                                        36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98012318; PubMed=9454068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833 840 ATE 1616 AA: 183614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 292909; CAB07439.1; ..
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                                                                                                                                                                            49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA REPLICATION.
       1727 AA;
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 VNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=138312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 VEIQKOTV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
NP_BIND
SEQUENCE
       SEQUENCE
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RRPO_TOMK2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRPO_TOML STANDARD; PRT; 1616 AA.
P03597; 041352;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation 
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 EEP-SIRGSMARGELQLAGLSGDVPESSYTRSEEIESLEGFHMATASSLIHKQMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 MTAAKVIVAVMSNESGLTLTFEUPTEANVALA------LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13] HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 188
                                                                                                                                                                                                                                                                                                                                                     536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
9.3%; Score 98.5; DB 1; Length 1616;
20.4%; Pred. No. 4.9;
Eve 44; Mismatches 79; Indels 33; Gaps
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                                                                                                                                                                                                                                       23 KLKVDLGVLQKSSAWQLAKQKAQEAFKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and comparison with the common strain genome."; J. Riochem. 96:1915-1923(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLIRANSFERASE/RNA HELICASE.
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W; A8EC8929B5CF7CAF CRC64;
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InterPro: IPR002588: V_methyltransf.
InterPro: IPR00606; Viral_helicasel.
Pfam, PF00978; RNA_dep_RNApol2; 1.
Pfam; PP01443; Viral_helicasel: 1.
Pfam; PF01660; Vmethyltransf: 1.
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                                                                         20.4%;
                                                                                                                                40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 YTGPLKVQQMKNFIDS 712
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1616 AA;
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                                                                               Best Local Similarity
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SEQUENCE
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                        Query Match
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                                                                                                                                            Matches
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Score 98.5; DB 1; Length 1616;

9.38;

Query Match

9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09YXD6: 09WJ37;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (183 KDa protein) (Contains: Methyltransferase/RNA helicase (MT/HEL) (126 KDa protein)].
Tomato mosaic virus (Strain S-1) (TOWY).
Viruses; SSRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
-:- MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                    589 MTAAKVIVAVMSNESGLILITEQPITEANVALA-----LQDSEKASDGALVVTSKDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                      131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL RNA REPLICATION.
                                                                                                        23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKI.LPTNTDIFGLKISNSLII.DVKAEP 82
                                33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhōu X., Xue C., Chen Q., Qi Y., Li D.; "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
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METHYLTRANSFERASE/RNA HELICASE.
                                79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
W: 5DBBFB2FADCC5C0C CRC64;
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20.4%; Pred. No. 4.9; ive 44; Mismatches
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InterPro: IPR001708; RNA_dep_RNApol2.
InterPro: IPR002688; V_methyltransf.
InterPro: IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00978; RNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ132845; CAB36997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01660; Vmethyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 YTGPLKVQQMKNFIDS 712
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          833 8,
1616 AA;
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=138314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
SEQUENCE
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                                            Matches
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23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82

9.3%; Score 98.5; DB 1; Length 1616;

Pred. No. 4.9;

20.4%;

Query Match Best Local Similarity

Mismatches

44;

40; Conservative

Matches

ò

Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHWATASSLIHKQMCSI--V 696
: | 1: | : | 1: | 1: | 589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA-----LQDSEKASDGALVVTSRDV 639
                                                       83 IDDGK------GLNI,SF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLJRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDELINE-95350630; PubMed-7542800;
MEDELINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
LIGN OR LIG OR HI1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {decoxyribonucleotide}(M) = AMP + nicotinamide nucleotide +
decoxyribonucleotide() (MM).
-! SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY.
-! SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}\,.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001679; DNA_ligase_N.
InterPro; IPR004150; DNA_ligase_OB.
InterPro; IPR004149; DNA_ligase_2BD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000445; HHH.
IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001357; BRCT
                                                                                                                                                                                                               189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                  697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                              DNLJ_HAEIN
P43813;
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InterPro;
InterPro;
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SEQUENCE
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                                                                   DOMAIN
                                                                               DOMAIN
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                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                     294 IDGTVLKINDIALQNELGFISKAPKWALAYKFPAQEELTLLNDVEFQVGRTGAITPVAKL 353
                                                                                                                                                                                                                                                                                                                                                                        | : |: :|| : || 354 EP--vFVAGVTVSNATLHNG-----DEIERLNIAIGDTVVIRRAGDVIPQII------ 398
                                                                                                                                                                                                                                                                                                                                                         59 LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDL 118
                                                                                                                                                                                                                                                                                                                                                                                                                119 LTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                          399 --GVLHERRPDNAKPIIF-----PTNCPVC----DSQIIRIEGEAVARCTGGLFCAAQ 445
                                                                                                                                                                                                                                                                           52; Gaps
                                                                                                                                                                                                                                                                                                      13 VDNTLKGILE-KLKVDLGVLQVSSAWQLA-KQKAQEAEKLLNNV------1SKL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                  PROSITE; PS50172; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
Ligsse; DNA_repair; DNA_replication; NAD; Complete proteome.
DOMAIN 601 679
BRCT.
                                                                                                                                                                                                                                              Query Match 9.0%; Score 95; DH 1; Length 679:
Best Local Similarity 24.5%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                           e8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQ38_CAEEL STANDARD; PRT; 1531 AA. 009459; Q09513; C.-NOY-1997 (Rel. 35, Created) C1-NOX-2002 (Rel. 41, Last sequence update) C1-MAR-2002 (Rel. 41, Last annotation update) Hypothetical 174.9 kDa protein C09G5.8 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2:
Palmer S., Sulshon J.;
submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          AMP (BY SIMILARITY).
4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO C.ELEGANS 2K666.1 AND 2K666.4.
                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 QKEICPLIRIFI--HSLDVN-----VIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| :: |: :: |: :| : | 446 RKE---ALKHFVSRKAMDIDGVGGKLIEQLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                  Probom; PD003944; DNA_ligase_N; 1.
SMART; SM00292; BRCT; 1.
SMART; SM00278; HhH1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 246791; CAA86762.2; -.
EMBL; 246792; CAA86762.2; JOINED.
 Pfam; PF01653; BKCT; 1.
Pfam; PF01653; DNA_119ase_N; 1.
Pfam; PF03120; DNA_11gase_OB; 1.
Pfam; PF03119; DNA_11gase_ZBD; 1.
Pfam; PF00633; HHH; HH; 1.
                                                                                                                                                                                             125 125 A
679 AA; 75188 MW;
                                                                                                                                                                                                                                                                             52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / AB972;
Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venema J., Tollervey D.; "RRP5 is required for formation of both 18S and 5.8S rRNA in yeast."; EMBO J. 15:5701-5714(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 -----LDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 THQPVAVLGECASD-----PTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEIC 183
                                                                                                                                                                                                                                                                                                               Match
Local Similarity 24.9%; Pred. No. 8.7;
es. 65; Conservative 33; Mismatches 73; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLEPVLHEGLETVDN-------TLKGILEKLK-VDLGVLQKSSAWQLAKQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 K-----IFGLKISNSL1---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 15:5701-5714(1996).
-! FUNCTION: INVOLVED IN THE BIOGENESIS OF RRNA. REQUIRED FOR THE FORMATION OF 18S AND 5.8S RRNA.
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-!- SIMILARITY: CONTAINS 4 HAT REPEATS.
-! SIMILARITY: CONTAINS 1 151 MOTIF DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryola, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                           1150 1154 POLY-ASP.
1531 AA; 174862 MW; A453990AF0DEBC2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1729 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rRNA biogenesis protein RRP5.
RRP5 OR FM11 OR YMR229C OR YM9959.11C.
                                                                                                                             POLY-SER.
POLY-ASN.
POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHÁRACTERIZATION.
MEDLINE≃97051828; Pubmed=8896463;
EMBL; 246792; CAA86767.2; -.
EMBL; 246791; CAA86767.2; JOINED.
WornPep; C09G5.8; CE25774.
Hypothetical protein.
384 394 POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 TL-----RYEIEVSQPISDS 875
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Q05022;
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Purnelle B., Skala J., van Dyck L., Goffeau A.; "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene and four new open reading frames including a leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 PRVKEEKKKVESNIEDPVDSSIKSWDDLS-----IGSIV---KAKIKSVKKNQLNVILA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 -----VTVAGPIIGQIINLKA----SLDL------LTAVTIETD------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                     687 DTIENIVPGRTIITVHVIEKTKDSVIVEIPDVGLRGVIYVGHLSDSRIEONRAOLKKLRI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747 GTELTGLVIDK--DTRTRVFNMSLKSSLIKDAKKETLPLTYDDVKDLNKDVPMHAYIKSI 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 805 SDKGLFVAFNGKFIGLVLPSYAVDSRDIDISKAFYINQSVTVYLLRTDDKNOKFLLSLKA 864
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              11 ETVDNTLKG-----ILEKLK------VDLGVLQKSSAWQLAKQ--KAQE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 AEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPI----DDGKGLNLSFPVTAN---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00N-1994 (Rel. 29, Created)
01-00N-1994 (Rel. 29, Last sequence update)
01-0NN-1994 (Rel. 29, Last annotation update)
Hypothetical 118:9 % Da protein in PTMI-IXRI intergenic region.
                                                                                                                                                                                                                                                                                                                                                                         8.9%; Score 94.5; DB 1; Length 1729; 20.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                      44; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                     193133 MW; 39BF46E5587B3B0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1038 AA.
                                                                                                                                   SI MOTIF 1.
SI MOTIF 2.
SI MOTIF 3.
SI MOTIF 4.
SI MOTIF 6.
SI MOTIF 6.
SI MOTIF 7.
SI MOTIF 9.
SI MOTIF 10.
SI MOTIF 11.
HAT 1.
                                                                                                                        Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94262309; PubMed=8203146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 IFIHS-LDV----NVIQQVVDNPQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            916 ANLHGRVDIAEVFDTYEE1TDKKQ 939
                                                                             SMART; SM00366; HAT; 2.
SMART; SM00316; SI; 12.
PROSTE; PS50126; SI; 11.
Nuclear protein; rkNA processing;
EMBL; Z49939; CAA90200.1; -. HSSP, P05555; ISRO. SGD; S0004042; RRP5. InterPro; IPR003107; HAT. InterPro; IPR003107; HAT.
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 20.5%
hes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                               1083
1159
1245
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1487
1594
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676
769
863
971
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                                                                   Pfam; PF00575; S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                       1265
1455
1561
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P36097;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 VKAEPIDDGKGLN---LSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 IKVNKLTDIRELSDTKLKHEINQSFMFNGPI-------VLLRTDGKTHKDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AVLGECASDPTSISL----SLLDKHSQIINK----FV-----NSVINTLKSTVSSL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 VLHQFFKSVRSQRYHKEFFSNSKPNLLPALGHSVTILLKILEQSPQNNELOFKALASLEV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VLHEGLETV-------DNTLKGILEKLKVDLGVLQKSSAWQLAKQKA-QEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein and a homologue to the yeast mitochondrial regulator ABE2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycet
                                                                                                Submitted (MAR-1994) to the EMBL/Jeenbaun, www. ---- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Mypothetical 108.2 kDa protein in SAP4-OST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%; Score 93.5; DB 1; Length 1038;
11.4%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 7;
46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 D068AEC2F4556A72 CRC64;
                                                                                            (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 LOKEICPLIKIFIHSLDVNVIQQVVDNPQHK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 VHLEKDPMSKLPSHLVK---LKEVVNEDLHK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 LLNNVISK-----LLPTNTDIFG------
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                              Transmembrane
                                                                                                                                                                                                                                                                                         EMBL; X71622; -; NOT_ANNOTATED_CDS.
EMBL; Z28033; CAA81868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kramer B., Kramer W.;
                                                                                                                                                                                                                                                                                                                                                                                                                 594 610 POT:
869 885 POT:
1038 AA; 118888 MW;
                                                            SEQUENCE OF 913-1038 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 21.4 Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                            PIR; S37854; S37854.
SGD; S0001516; YKL033W.
                                                                                                                                                                                                                                                                                                                                                     SGD; Suverier, Hypothetical protein; T
                        reast 10:125-130(1994).
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P53076;
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90178: Q90177:
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence (EC 2.7.7.48) (183 kDa protein) (Contains: Mathyltransferase/RNA helicase (EC 2.7.7.48) (183 kDa protein) (Contains: Methyltransferase/RNA helicase (MY/HE) (126 kDa protein))
10-OCT-2001 (Rel. 40, Last and viruses; ssrNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 LNLS----FPVTANVTVAGPLIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 QELSNEFIYDTKIPQSLRDRFSGQLSNVSALL-----AYSNPLVEAPKEISGYLSDEY 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778 YLINKGQISKCINYIDNEIPDLLKNNLELVFELKLANYLVMIKKSSSKDDDEIENLILKG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Tobacco Mosaic virus.";
Mol. Biol. (Mosk) 34:172-176(2000).
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 LIHEGLVDV---AKGFLKDLQKDAVNVNGQHSESKDVIRHNER-QIMKEERMVKIRQELR 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196905; PubMed-10732356; Belenovich E.V., Novikov V.K., Zavriev S.K.; "Biological properties and genome structure of the Kazakh isolate Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VLHEGLETVDNTLKGILEKLKVDL-------GVLQKSSAWQLAKQK----AQEAE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 KLLN------NVISKLLPTNTD-IFGLKISNSLILDVKAEPIDDG------KG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 22.8%; Pred. No. 7.6;
Matches 51; Conservative 39; Mismatches 71; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
; 335ADD152949F8C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 -----PTSISLSLEDKHSQIINKFVNSVINTLKSTVSSLLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 LQERLFQVSNYTILTFLHKDSECA---LENVISNTRAMLSTLLE 931
                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ASP.
                                                                                                                                                                                                                  SGD; S0003196; VID30.
InterPro: IPR003877; SPRY.
InterPro: IPR003878; SPRY_domain.
Pfam; PF00622; SPRY; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           450 453 PO
958 AA; 108178 MW;
                                                                                                                                                                                            EMBL; 272749; CAA96943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                 165
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SEQUENCE
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131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 EEP-SIRGSMARGELQLAGLSGDVPESSYTRSEEIESLEGFHMATASSLIHKOMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKTSDKFDVDVFSOMCOSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 IDDGK-----GENLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 92
                                                                                                                                                                                                              Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1 1116 METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                   Watch 8.7%; Score 92.5; DB 1; Length 1616; Local Similarity 19.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             indels
                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
W; 4BF9913CE791DE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
EMBL, AJ243571; CAB62911.1; ...
EMBL, AJ243571; CAB62912.1; ...
Interpro: IPR001788; RNA_dep_RNApol2.
Interpro: IPR001288; V_methyltransf.
Interpro: IRR0U606; Viral_helicase1.
Pram; PP00978; RNA_dep_RNApol2; 1.
Pram; PF01443; Viral_helicase1; 1.
Pram; PF01460; Wnethyltransf: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 6, 2002, 17:07:34
                                                                                                                                                                                                                                                                                                                              1616 AA; 183606 MW;
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SEQUENCE
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August 6, 2002, 17:09:28 ; Search time 111.35 Seconds (without alignments) 334.027 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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sp_human:*
sp_invertebrate:*
sp_marmmal:*
sp_marmel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 200000000
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sp_virus:*
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                                                                                                                                                                                Title:
Perfect score:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09bqq0 homo sapien 096dr5 homo sapien p79124 hos taurus p79125 hos taurus p79125 hos taurus p79125 hos taurus p63471 rattus norv p63471 rattus norv p6350 rattus norv p9dpp2 mus musculu p9dp4 mus musculu p9dp9 mus musculu p9dpp8 homo sapien p64114 mus musculu p9dpp8 homo sapien p9dpp8 homo sapien p9gp31 staphylococ
SUMMARIES	098000 096085 979124 09734 063471 063550 090692 090692 090690 091114 099058
DB	. 44 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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% Query Match	
Score	1061 10061 2 3 3 3 3 10061 2 2 9 9 3 3 3 5 5 3 1 10061 1 1 2 4 4 6 8 6 7 5 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Result No.	11111111111111111111111111111111111111

Oy Db oy Db

181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215

099110 tomato mosa 059040 methanococc 09403 tobacco mos 091004 tobacco mos 091004 tobacco mos 091108 tomato mosa 0911109 tomato mosa 091109 tomato mosa 091109 tomato mosa 091109 tomato mosa 09100 mus musculu 09200 mus musculu 09200 mus musculu 09400 mus musculu 09670 mus musculu 09500 musculu 09	Q e	FAEKLLNNVISKLLP 60 
0991T0 059040 094M0GS 09JA03 09JA04 099JR9 099JR9 091JR9 091JR9 091JR9 091JR9 091JR9 091JR9 091JR9 091JR9 091JR9 091ZG8 091ZG8 091Z91	ALIGNMENTS  INARY; PRT; 249 AA.  Lrel. 17, Created) Lrel. 19, Last sequence update) TO BOVINE SALIVARY PROTEIN BSP30).  n). Chordata; Craniata; Vertebrata; E; Primates; Catarrhini; Hominidae; primates; Catarrhini; Hominidae; 27011 MW; E64E0794A1B4DB7D CRC64 27011 MW; E64E0794A1B4DB7D CRC64 27011 MW; E64E0794A1B4DB7D CRC64 27011 WW; Roore 1061; DB 4; Len 100.0%; Score 1061; DB 4; Len 100.0%; Pred. No. 9.2e.78; vative 0; Mismatches 0; Ind	KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 
	NARY; Fel. 17, Crefel. 17, Lastel. 19, Lastel. 19, Lastel. 19, Lastel. Obovine S). Chordata; Cho	KGILEK         KGILEK
11116 866 11186 1016 1016 1016 1016 1016	PRELIMINARY;  (Tremblrel 1 (Tremblrel 1) (Tremblrel 1) (Tremblrel 1) SIMILAR TO BOV S (Human).  S (Human).  Metazoa; Chord Wetazoa; Prima Outheria; Prima Outh	IVDNTE I
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TISSUEFFICIAL SCREEN, Wheeler T.T.;
Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a Lovine member of the Parctid Secretory Protein family.";
Submitted (NV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79414, AAB38283.1;
SEQUENCE 240 AA: 26513 MW; 850611DE9E43E358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TNTD1FGLK (SNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPI1GQ11NLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TDPQTHQPVAVLGECASDPTS1SLS1,LDKHSQI1NKFVNSVINTLKSTVSSLLQKEICPL 185
                                                                                                                                                                                                                                                                              87 VVSRLTGVRIRNVQVPDITFEATSENSA-NVLIPITADVIVSLPFLGEIVDLDLNVDLQT 145
                                                                                                                                             66 FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                             6 LHEGLETVUNTEKGILEKLKVINGVIQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDI 65
                                                                             32 KIKSGLERGLDTFDSTIEIIFONLKTE---LESRCSDEVVEQ--QETENFLEQLISRIFQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
78;
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 ELCPRFRELLESLDAECVEKLIGESQDTTQ 233
                                                                                                                                                                                                                                                                                                                                                    186 IRIFIHSLDVNVIQQVVDNPQHKTQLQT 213
                                                                                                                                                                                                                                                                                                                                                                                                    212 IRELLESIDTECIKKLIGEPOVTTOUES 239
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71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 33.8%
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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     Matches
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"The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79413; AAB382821;
SEQUENCE 243 AA; 26877 MW; 0C2D8DD45660E11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF432917; AAL28113.1; -.
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASI,DI.LT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ1INKFVNSVINTLKSTVSSI.LQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AVTIETDPQTHQPVAVLRECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLJOK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNV1SKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 KLEPVLHEGLETVDNFLKGILEKLKVDLGVLGKSSAWQLAKQEAEKLLNNVISKLLP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Wakaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Perora: Rovoldea:
Bovidae: Bovinae: Bos.
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 1053; DB 4; Length 249; 99.5%; Pred. No. 4.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 EICPLIRIFIHISLDVNVIQQVVDNPQHKTQLQTLI 249
     215 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTL1 249
                                                                                                                                   249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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01-MAY-1997 (TrEMBLrel. 03, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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34.1%;
                                                                                                                                                                                                                                                           PAROTID SECRETORY PROTEIN.
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                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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Best Local Similarity
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protein are alternatively regulated members of a salivary protein
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KANAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kayai J., Shinaqawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A aizawa T., Hara A., Fukunishi Y., Konno H., Kando S., Yamanaka I.,

Kaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Futuno M., Aono H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Nordone W., Kawaji H., Kohtsuki S.,

Rayanaki W., Rayanaki W., Kawaji H., Kohtsuki S.,

Rayanaki W., Rayanaki W., Kawaji H., Kawaji H., Kawaji W.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92129360; PubMed-1370829;
Mirels L., Ball W.D.;
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 SKLLPTNTDIFG--LKISNSL1LDVKAEPIDDGKGLNLSFPVTANVTVAGP11GQ1INLK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ASI.DI.I.TAVTTETDPQTHQPVAVLGECASDPTS1.SI.I.DKHSQ11NKFVNSV1NTI.KST 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 LGNLKSFTSLNGLLLKINNLKVLDFQAKLSSNGNGIDL/TVPLAGEASLVLPFIGKTVDIS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EPVLHEGLETVDNTLK------GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%; Score 294.5; DB 11; Length 235; 32.7%; Pred. No. 4.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AA; 24737 MW; A29D0160268DA0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) NEONATAL SUBMANDIBULAR GLAND PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001
 Mus musculus (Mouse)
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Best Local Similarity
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                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
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"Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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0B36EC779025986E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
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"Characterization of the rat salivary-gland Bl-immunoreactive
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MEDLINE-98129760;
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multigene family.";
J. Bjol. Chem. 267:2679-2687(1992).
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235 AA; 24529 MW;
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XX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Izawa M., Ashburner M., Batalov S., Casavant T.,

XA Sato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

XA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

XA Schriml L.M., Staubli F., Suzuki R., Tomital M., Magner L., Washio T.,

XA Sakai K., Okido T., Fuuno M., Aono H., Haddarelli K., Barsh G.,

A Blake J., Boffelli D., Hojunga N., Carninci P., de Bonaldo M.F.,

A Browstein M.J., Bult C., Fletcher C., Fullta M., Kamiya M., Lee N. H.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Sasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

XA Sasaki H., Zato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                               DB 11; Length 206;
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EMBL, AKO10143; BAB26728.1; -.
MGD; MGI:1919667; 2310074B19R1k.
SEQUENCE 235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
                                                   91C001620761067B CRC64;
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01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
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                                                                                                                                                                                                               14.6%; Score 154.5; DB 1
24.5%; Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                       42; Mismatches
CELL PROTEIN.
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                                                   206 AA; 23027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 LIISN---TFHPDEISNPQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 IFTHSLDVNVIQUVVDNPQ 206
                                                                                                                                                                                                                                                                   Best Local Similarity 24.5%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2310074B19RIK PROTEIN.
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Antanawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Enkuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Enkuda S., Alawa K., Izawa M., Nishi K., Kino B., Kamaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Baralov S., Casavant T., Ashburner M., Baralov S., Casavant T., Ashburner M., Ring B., Kochiwa H., Ashburner M., Ring B., Kochiwa H., Sakuli F., Suzuki R., Tomita M., Wagner L., Washlo T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bronstein M.J., Boliunga N., Carninci P., de Bonaldo M.F., Abronstein M.J., Boliunga N., Carninci P., de Bonaldo M.F., Abronstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
132 LELSVKLDVTAEVYAVRDSYGKSKL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 148.5; DB 11; Length 270; 25.3%; Pred. No. 0.00029; Live 38; Mismatches 74; Indels 3;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                        170 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 203
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN~C57BL/6J; TISSUE-TONGUE;
MEDLINE~21085660; PubMed~11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1914385; 2310021H06Rik.
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EMBL; AK009441; BAB26290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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01-JUN-2001 (
01-JUN-2001 (
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EMBL; AK010145; BAB26730.1;
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 46; Conserva
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                                         SEQUENCE FROM N.A.
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Stranger 1, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Shinagawa A., Shibata K., Yonoo H., Adachi J., Fukuda S., A Arakawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kashawa T., Saito R., Ashurrer M., Baralov S., Casavant T., Rackenann W., Gaasterland T., Gissi C., King B., Kochiwa H., Racken M., Saito R., Ashurrer M., Maralov S., Casavant T., Racken M., Staubi F., Suzuki R., Tomital M., Wagner L., Washio T., Ashur M., Staubi F., Suzuki R., Tomital M., Wagner L., Washio T., Rakai K., Okido T., Pouro M., Aono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F., Ruonstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Norlone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Antono P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whythaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Anachioaki Y., Kawaji H., Kohtsuki S.,
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ص
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 VLGKVISS-IPLENNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                        'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492A16EEBAB4A677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310021H06FIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 148.5; 1
25.3%; Pred. No. 0.000
Live 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1914385; 2310021H06Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAB26360.1; -. BAB26372.1; -. BAB26401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AK010115; BAB26710.1; -. AK009329; BAB26221.1; -. AK009531; BAB26343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK009695; BAB26444.1; -. AK009803; BAB26513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK009835; BAB26533.1; -. AK010012; BAB26642.1; -. AK010051; BAB26667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
2310021H06RIK PROTEIN.
                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 AA;
                                                                                                    SEQUENCE FROM N.A.
                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK009562;
                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2310021H06RIK.
             2310021H06RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
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EMBL;
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A STRAIN-C57BL/63; TISSUE-TONGUE;

A MANAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Marawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Shinagawa A., Shibata K., Yonoo H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki T., Gojobori T., Bono H., Kashawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Radota K., Matsuda H., Saito Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Radota K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Radota K., Sato K., Kang K.H., Weitz C., Whittaker C., Wilming L.,

Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Radota K., Mang K.H., Mester C., Whittaker C., Wilming M.,

Radota K., Mang K.H., Weitz C., Whittaker C., Wilming M.,

Radota K., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota K., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota K., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota K., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota K., Wang K.H., Weitz C., Whittaker C., Wilming M.,

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Radota M., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota M., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota M., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota M., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota M., Wang K.H., Weitz C., Whittaker C., Wilming M.,

Radota M., Wang K.H., Weitz C.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO DNA SEGMENT, CHR 2, MASSACHUSETTS INSTITUTE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008429; AAH08429.1; -.
SEQUENCE 484 AA; 52427 MW; 08242B697284E858 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1914385; 2310021H06Rik.
SEQUENCE 270 AA; 29235 MW; A86F02ABBAAFBCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 145.5; DB 11
25.3%; Pred. No. 0.00051;
tive 38; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 LKSTVSSLLØKEICPLIRIFIHSLDVNVIQQVVD 203
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                  72 NSLILDVKAEPIDDGKGLNLSFPVTANVTVAG---PIJGQIINLKASLDLLTAVTIETDP 128
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ches 76; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VEHEGLETV------DNT1/KG1LEKLKVDLGVLQKSSAWQLAKQKAQEAEKI,LNNVI 55
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
18 KGILEKLKVUI,-----GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 AA; 52373 MW; 377DBFA5E736709B CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01:JUN-2001 (TrEMBLrel. 17, Last annotation update)
1700058CI3RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 17, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U46068; AAA87581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SWISS-WEBSTER;
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Q9D9J8;
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STRAIN-CSTBL/63; TISSUE-TESTIS;

MEDLINE-21085660; Pubbled-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A satawa K., Izawa M., Nishi K., Konno H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Kuchl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Ouackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rasai K., Okido T., Furuno M., Aon H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasai H., Sato K., Wang K., Wang K.H., Wettz C., Whittaker C., Wilming L.,

Wanshay-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AEPIDDGKGLNLSFP---VTANVTVAG-----PIIGQIINLKASLDLLTAVTIETDPQT 130
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49C10.6 (SIMILAR TO MURINE VON EBNER MINOR SALIVARY GLAND PROTEIN,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AI,121901; CAC03550.1; -.
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EMBL; AK006829; BAB24760.1; -.
MGD; MGI:1920638; 1700058C13Rik.
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Mus musculus (Mouse).
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                                                               NCBI_TaxID=10090;
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Search completed: August 6, 2002, 17:09:29 Job time: 931 sec

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August 6, 2002, 16:52:52; Search time 138.55 Seconds (without aliquments) 172.363 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*

## SUMMARIES

						•					
Description	Human parotid secr	Human parotid secr	Human PRO1025 prot	Human secreted pro	Human secreted pro	Human protein sequ	. Peptide #8941 enco	Human brain expres	Human bone marrow	Peptide #9264 enco	Mouse 28.6 kDa sec
ID	AAW69221	AAW60682	AAB24069	AAB25765	AAB75351	AAM25745	ABB41435	AAM62308	AAM75111	AAM35227	AAE05367
DB	19	19	21	21	22	22	22	22	22	22	22
Length	249	249	249	249	249	260	20	20	20	50	278
% Query re Match Length DB ID	100.0	100.0	100.0	100.0	100.0	96.4	23.2	23.2	23.2	23.2	17.2
Score	1061	1061	1061	1061	1061	1023	246	246	246	246	182.5
Result No.	-	7	e	4	S	9	7	αο	σ	10	11

(HUMA-) HUMAN GENOME SCI INC.

Duan R, Ruben SM;

97WO-US23522. 96US-0034429.

18-DEC-1997; 23-DEC-1996;

12   178   16.8   256   20   AAV06408   Human secreted pro								
178   16.8   256   20   AAM95463   LS170 polly     178   16.8   256   22   AAV3919   AAV3919     178   16.8   264   22   AAV3919   AAV3919   AAV3919     178   16.8   264   22   AAV3919   AAV3919   AAV3919     18   18   22   AAV3919   AAV3919   AAV3919     18   18   22   AAV3919   AAV3919   AAV3919     14   13.6   484   22   AAV3919   AAV3919   AAV3919     14   13.6   484   22   AAV3919   AAV3919   AAV3919     14   13.6   484   22   AAV3919   AAV3919   AAV3919     18   18   29   29   22   AAV3919   AAV3919     18   18   29   29   22   AAV3919   AAV3919     18   29   29   29   29   29   29     19   29   29   29   29   29     10   20   20   20   20     20   30   30   30   30     30   30   30	1,0	178	3,41	256	20	4	Human	ecreted pr
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178   16.8   256   22   AAU 29210   Human Section   178   16.8   256   22   AAU 29210   Human Section   178   16.8   256   22   AAU 29210   Human DOLV   178   16.8   256   22   AAM 92212   Human DOLV   178   16.8   264   22   AAM 92209   Human DOLV   178   16.8   264   22   AAM 92209   Human DOLV   168   16.8   264   22   AAM 92214   Human DOLV   168   16.8   264   22   AAM 92214   Human DOLV   169   16.8   264   22   AAM 92214   Human DOLV   146   13.8   484   21   AAY 9375   Human DOLV   144   13.6   484   21   AAY 9375   Human DROL   144   13.6   484   22   AAB 66220   Human PROL   144   13.6   484   22   AAB 66220   Human PROL   144   13.6   484   22   AAB 66220   Human PROL   144   13.6   484   22   AAB 66220   Human DROL   144   13.6   484   22   AAU 34336   Staphylocc   275   22   AAU 34336   Staphylocc   275   2710   174   275	2 -	170	0.01	2 4 5	, ,		O C L E A	acid segment
178   16.8   256   22   AAM39721   Human PRON     178   16.8   256   22   AAM39721   Human PRON     178   16.8   256   22   AAM39721   Human PRON     178   16.8   264   22   AAM9220   Human Doly     178   16.8   264   22   AAM9220   Human Doly     178   16.8   264   22   AAM41807   Human Doly     178   16.8   264   22   AAM41807   Human Doly     178   16.8   264   22   AAM4721   Human Doly     179   13.8   318   22   AAM4721   Human Doly     146   13.8   310   22   AAM4721   Human Doly     147   13.6   484   21   AAY7126   Human Doly     148   13.6   484   22   AAB87564   Human PROI     149   13.6   484   22   AAB87564   Human PROI     140   13.6   484   22   AAB87564   Human PROI     141   13.6   484   22   AAB87564   Human PROI     141   13.6   484   22   AAB87564   Human PROI     142   13.6   484   22   AAB87564   Human PROI     183   126   22   22   22   22   22     184   22   23   23   24   24     185   299   22   22   24     186   2710   17   AAR8938   C. dificil     186   2710   17   AAR8939   C. dificil     186   2710   17   AAR8939   C. dificil     187   22   22   24   24     289   2478   22   AAB8838   C. dificil     291   292   292   292   292   292     292   293   293   293   293     293   293   293   293   293   293     294   295   293   293   293     294   295   293   293   293     295   295   293   293   293     295   295   295   293   293     295   295   295   295     295   295   295   295     295   295   295   295     295   295   295   295     295   295   295   295     295   295   295   295     295   295   295   295     295   295   295     295   295   295   295     295   295   295   295     295   295   295   295     295	4.	710	0.0	7 10	7 (	- 0	0 4 5 5 5	coores ad pro
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167   15.7   191   22   AAM92214   Human dige   146   13.8   318   22   AAM47220   Human NOVE   146   13.8   318   22   AAM47220   Human NOVE   146   13.8   484   21   AAV77126   Human NOVE   144   13.6   484   22   AAG53976   Human NOVE   144   13.6   484   22   AAG53976   Human PROJ   Human PROJ   144   13.6   484   22   AAB6524   Human PROJ   Human PROJ   Human PROJ   144   13.6   484   22   AAB6524   Human PROJ   Human PROJ   Human PROJ   13.5   565   22   AAB66124   Protein Of   Protein Of   168   10.2   121   AAR66139   Human PROJ   Human PROJ   169   160   170   170   AAR66139   Human PROJ   Human PROJ   160   170	0 2 5	0 7 1	o u	187	2 0	AAM92212		digestive sv
46   13.8   318   22   AAM47220   Human NOV6   146   13.8   320   22   AAM47224   Human NOV6   146   13.8   320   22   AAM47224   Human NOV6   146   13.8   320   22   AAM77224   Human NOV6   144   13.6   484   22   AAG63976   Human PRO1   144   13.6   484   22   AAB67564   Human PRO1   144   13.6   484   22   AAB67564   Human PRO1   143   13.5   52   22   AAG68220   Human PRO1   108   10.2   197   21   AAR66124   Protein of	22	167	าเ	100	4.0	AAM92214		digestive sy
146   13.8   320   22   AAM47214   Human NOV6   146   13.8   484   21   AAY77126   AM1000 acid   145   13.6   484   21   AAY9375   AAG6376   AM100 acid   144   13.6   484   22   AAG6376   AM100 acid   144   13.6   484   22   AAG6376   Human PRO	22	145	າ.~	318	2.5	AAM47220		NOV6b protei
146   13.8   484   21   AAY7126   Human neur   145   13.7   484   22   AAG3976   Amino acid   144   13.6   484   22   AAV99375   Human PRO    144   13.6   484   22   AAV9975   Human PRO    144   13.6   484   22   AAB6524   Human PRO    Human PRO    144   13.5   565   22   ABG6524   Human PRO    Human Hum	24	146	· ~	320	22	AAM47214		NOV6a protei
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144   13.6   484   21   AAV99175   Human PROI   144   13.6   484   22   AAU9163   Human PROI   144   13.6   484   22   AAB67564   Human PROI   143   13.5   484   22   AAB66124   Human PROI   143   13.5   52   22   AAG66124   Novel human PROI   108   10.2   13.7   21   AAR86219   Human Secritor   108   10.2   221   21   AAR86219   Human Secritor   221   21   AAR86219   Human Secritor   221   22   23   23   24   AAR86068   Human Secritor   23   22   23   23   23   23   24   23   24   23   24   24	26	145	~~	484	22	AAG63976		acid sequenc
144   13.6   484   22   AAU29163   Human PRO   144   13.6   484   22   AAB6124   Human PRO   144   13.6   484   22   AAB6124   Human PRO   143   13.5   565   22   ABC08220   Human PRO   Human PRO   10.2   13.7   13.6	27	144	m	484	21	AAY99375		PRO1357 (UNQ
144   13.6   484   22   AAB67564   Human PRO1   144   13.6   484   22   AAB66124   Protein OF 144   13.6   56.5   22   AAB66124   Protein OF 168   10.2   19.7   21   AAR66139   Human secritical Se	28	144	$^{\circ}$	484	22	AAU29163		PRO polypept
144   13.6   484   22   AB665124   Novel human 13.5   55.5   22   AA786219   Novel human 10.2   10.2   10.2   22.1   AA86219   Human secritors   10.8   10.2   22.1   AA866124   Novel human 10.2   10.3   22.1   21.2   AA866124   Human secritors   22.1   22   22   22   22   22   22	58	144	m	484	22	AAB87564	Human	PRO1357. Ho
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69221 standard; Protein; 249		9221;						
69221 standard; Protein; 249 69221;	7	3661-15	`		( )			
#69221 AAW69221 standard; Protein; 249 AAW69221; 16-DCT-1098 (first entry)								
469221 AAW69221 standard; Protein; 249 AAW69221; 16-OCT-1998 (First entry)		n parot		retory	prot	ein.		
469221 AAW69221 standard; Protein; 249 AAW69221; 16-OCT-1998 (first entry) Human parotid secretory protein.		tid sec immune apy; di	defens lagnosis		orde	; digestive di immune system	er; endocri der; cance	ne disorder; r; human;
AAW69221 standard; Protein; 249 AA.  AAW69221; 16-OCT-1998 (first entry) Human parotid secretory protein. Parotid secretory protein; hPSP; digestive disorder; endocrine non-immune defensive disorder; immune system disorder; cancer; therapy; diagnosis.		sapier	Š					
AAW69221 standard; Protein; 249 AA.  AAW69221 standard; Protein; 249 AA.  AAW69221;  16-OCT-1998 (rirst entry)  Human parotid secretory protein.  Parotid secretory protein; hPSP; digestive disorder; endocrine non-immune defensive disorder; immune system disorder; cancer; therapy diagnosis.		2						
AAW69221 standard; Protein; 249 AA.  AAW69221; 16-OCT-1998 (first entry) Human parotid secretory protein.  Parotid secretory protein; hPSP; digestive disorder; endocrine non-immune defensive disorder; immune system disorder; therapy; diagnosis.  Homo sapiens.								

1..18 /note= "signal peptide" 19..249 /note= "mature hPSP" Location/Qualifiers WO9828420-A1 02-JUL-1998. Peptide Protein 

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This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and invention. The hPSP DNA is useful for chromosome identification and is consistent of hPSP (in standard blotting, and protein can be used to detect abnormal levels of hPSP (in standard blotting, and inmune defensive, endocrine or immune system disorders. A particular opportation is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral ayenessing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secretory tissue; gastrointestinal Lissue; HPSP, Sjorgen's syndrome; Graves disease, thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1061; DB 19; Length 249; 100.0%; Pred. No. 7.7e-93; Live 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW60682 standard; Protein; 249 AA.
                                                                                                                                  Claim 16; Fig 1; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hPSP-binding proteins.
WPI; 1998-377651/32.
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                     N-PSDB; AAV44759
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This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, eg. cancer of salivary gland, thyroid, gastrointestinal tract or pancreas, Sjorgan's syndrome, prostate, breast, gastrointestinal tract or pancreas, Sjorgan's syndrome, or grationtestinal tract or pancreas, Sjorgan's syndrome, or care to containing expression vectors comprising the HPSP nucleic acid are used containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells the express HSPP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used indicate cell proliferation. HPSP nucleic acid or its fragments are used to elect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; noctropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antianalogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
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                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1A-C; 65pp; English.
                 96US-0749288.
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                                                              (INCY-) INCYTE PHARM INC.
                                                                                                             Bandman O, Goli SK;
                                                                                                                                                          WPI; 1998-297933/26
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nes 215; Conserv
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PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, Kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AACS8242 to AACS8366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AACS8367 to AACS8368 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO535,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one of the human PRO proteins designated PR0212, PR0290, PR0341, PR0535, PR0619, PR0717, PR0809, PR0830, PR0848, PR0943, PR01005, PR01009, PR01003, PR01030, PR01037, PR01111, PR01135, PR01182, PR01187, PR01181, PR01218, PR0213, PR0339, PR0834, PR03117, PR01710, PR02094, PR02145 OR PR02198. PR0 antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer \cdot
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hypothalamic disorder; glandular disorder; macrophagal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated antibody
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99US-0145698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                   40200053755-A2.
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                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1999;
20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1999;
                                                                                                                                                                                                                                                                                                             14-SEP-2000.
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249 AA;
                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                               61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
                                                                                           0; Gaps
                                                                                                                                                    1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                  100.0%; Score 1061; DB 21; Length 249; 100.0%; Pred. No. 7.7e-93; ive 0; Mismatches 0; Indels 0;
                                                                         Best Local Similarity 100.
Matches 215; Conservative
249 AA;
                                                          Query Match
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95

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This sequence represents a human secreted protein amino acid sequence.

The invention relates to sequences AAA87725.858774 which encode human

Secreted proteins AAB25763.825812. The proteins include signal peptides.

Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the cDNA sequences to binding to one of the contained proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for dentifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The CDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amploidosis, brain disorders, skeletal muscle disorders, eye disorders, analyloidosis, microhondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, commentia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
215 eicplirifihsldvnviqqvvdnpqhktqlqtli 249
                                                                181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                     AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                  Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113686.
99US-0141032.
                                                                                                                                                                                                                                                                                                           28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides, useful in d
mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA87727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200037491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
25-JUN-1999;
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                                                                                                                                                                                                                                                                 AAB25765;
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61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120

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                                                                                                        TNTD1FGLK1SNSL1L,DVKAEP1DDGKGLNL,SFPVTANVTVAGP11GQ1INLKASLDLLT 120
                                                                                                                                                            121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 49 Secreted proteins and the CDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                   1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLCNNV1SKLLP 60
                                                                   49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1061; DB 22; Length 249; 100.0%; Pred. No. 7.7e-93; Live 0; Mismatches 0; Indels 0;
                           ..
0
DB 21; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; prevention; treatment; diagnosis; disease;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J, Bougueleret L, Jobert S;
                            ..
0
  Score 1061; DB 21
Pred, No. 7.7e-93;
                                                                                                                                                                                                                               215 eicplirifilisldvnviggvvdnpghktglgtli 249
                                                                                                                                                                                                                 181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                              AAB75351 standard; protein; 249 AA.
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2000; 2000WU-IB00951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99115-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0469099
                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 215; Conservative
    Query Match 100.0
Best Local Similarity 100.0
Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSE'F
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21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     infection.
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cells they are expressed in such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiinflammatory; antirheumatic; central nervous system; virucide; antiinflammostatic; entimatological; antianeomic; antiangorgant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polyuucleotides encoding them can be used in gene therapy, antisense therapy and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective, antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antiampsphylactic; rheumatoid arthritis; septic shock; pancratitis; cardiac dysfunction; neuropatchology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder: platelet disorder: asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antilnflammatory; antirheumatic; antiarthritic; immunosuppressive; antibocterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic;
95 tntdifglkisnslildvkaepiddgkglnlsfpvtanvtvagpilgginlkasidlt 154
                                                              121 AVTIETDPOTHOPVAYLGECASDPTSISLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                  Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and
                                                                                                                                                     181 EICPLIRIFIHSGAVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ 1D NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                           AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 2001-457603/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                            AAM25745;
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0; Gaps

1 KLEPVI,HEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLI,NNVISKLLP 60 

Matches

δ a Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English

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production, The proteins and polynucleotides are useful for screening for againsts or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HV and lungal infections, autoimmunity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                        TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 klepulhegletvdntlkgileklkvdlgvlgkssawglakgkageaekllnnviskllp 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                     1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                  96.4%; Score 1023; DB 22; Length 260; 96.7%; Pred. No. 3.4e-89;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eicplirifilisIdvnviggvvdnpghktglgtli 260
                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB41435 standard; Peptide; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                        neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                      260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
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                                                                                                                                                                                                                                                                                       208;
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB41435;
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                    Matches
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                              measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                 printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 34413; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                          0;
                             The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                             104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLID 153
                                                                                                                                                                                                                                                                                                                                              1 piigqiinlkasldlltavtietdpqthqpvavlgecasdptsislslld 50
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                      23.2%; Score 246; DB 22;
                                                                                                                                                                                                                                                                    100,0%; Preu...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM62308 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483446/52
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                         50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
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Best Local Sim
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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AAM35227 standard; Protein; 50 AA.
                                        (first entry)
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                                        17-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                    Gaps
                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                         Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ 1D NO: 35417; 658pp + Sequence Listing; English.
                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                       104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.2%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.2%; Score 246; DB 22; Length 50;
                                                                                 microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. nc.
                                   20.0%; Pred. ....
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                                                                                                                                               AA
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                                                                                                                                               AAM75111 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                        2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                               2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                 2000018-0236359
                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50; Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                         Best Local Similarity
Matches 50; Conserv
 50 AA;
                                                                                                                                                                                                                                                                                 WO200157276-A2.
                                                                                                                                                                                                                                                              HOMO Sapiens.
                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                    AAM75111;
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  Sequence
                                 Query Match
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AAM35227
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The present invention relates to single exon nucleic acid probes (SENP: see AA13115-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and dissplaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, cytostatic, antiinflammatory, immunoregulatory, tissue integrity, wound healing, immune response, vaccine, cancer, asthma, alleggy, cell trafficking, therapy, 28.6 kDa secreted protein.
Peptide #9264 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.2%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE05367 standard; Protein; 278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0652366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0256359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WP1; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50 AA;
                                                                                                       genetic disorder.
                                                                                                                                                                                                                                   WO200157272-A2.
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AAY06408

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process which play a major role in induction of growth, cell migration of proteins which play a major role in induction of growth, cell migration of tissue specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are of tissue integrity and thus are important in wound healing. They are arithodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or compounds, and as therapeutic target in a whole range of disease of their compounds, and as therapeutic target in a whole range of disease or states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynuclectices of the invention are useful for treating mammalian disorders. Polynuclectices of the invention or are useful in genome and physical mapping, in positional cloning of are useful in genome and physical mapping, in positional cloning of condistructure tags for marking organisms), and for the disgnosis and treatment of mammalian diseases which is the consequence of inappropriate capturent of a vaccine or anti-cancer treatment, as immunoregulatory and anti-inflammatory molecule, as a spart of a vaccine or anti-cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of the invention. For risane and plantal remembration, to promote or hinch the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is 28.6 kDa protein, a secreted protein from mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses novel polynucleotides and their corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 92; 101pp; English.
                                                                                                                                                                                                                   21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                            28-NOV-2000; 2000US-0724864.
                                                                                                                                                                                                                                                                                                                    99US-017167B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-425665/45.
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WO200148192-A1.
                                                                                                                                                                                                                                                                                                                    23-DEC-1999;
                                                                                                            05-JUL-2001
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85 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECAS 142
                                                                                                                                                                                                                    150 dghrlyvtiplgltlnvnmpvvgsllglavklnitaevlavkdnggrih---lvlgdcth 206
                                                                                                                                                                                                                                                                   143 DPTSISLELDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                         28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKL---LPTNTDIFGLKISNSLILDVKAEPID 84
                        DB 22; Length 278;
Ouery Match 17.2%; Score 182.5; DB 22; Length Best Local Similarity 24.5%; Pred. No. 3.1e-09; 45: Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                     203 DNPQHKTQ 210
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RESULT

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nh796_1. The sequence is predicted from a full-length cDNA clone (see AAX59356) isolated from a human adult brain (thalamus) CDNA library. The invention provides cDNA clones (see AAX59355.8) encoding novel secreted proteins (see AAX60404-10) of the human cestis, brain and foetal kidney. The polynucleotides and proteins are predicted to have blological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell crowth, activin or inhibin, chemotoctic or chemokinetic, hademostatic, thrombolytic, receptor/ligand, antiinflammatory, cacherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 igilenlplldilkpgggtsggllggllgkvtsvipglnniidikvtdpgllelglvqsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 DGKGINLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel human secreted protein, termed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 256;
                                                                                                                                     Secreted protein; nh796_1; human; brain; thalamus; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Indels
                                                                                                                                                                                                                                                    /note= "predicted leader/signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA, Jacobs K, LaVallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg D, Steininger RJ, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 24.5%; Pred. No. 7.5e-09;
Matches 46; Conservative 44; Mismatches 92;
                                                                                                                                                                                                                                                                                          "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                         Location/Qualifiers
AAY06408 standard; Protein; 256 AA.
                                                                                                    Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0222653.
98US-0070346.
                                                                                                                                                                                                                                                                                                                                                                                           98WO-US27903
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                          20..256
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                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                        W09935252-A2.
                                                                                                                                                                                                                                                                                                                                                                                           31-DEC-1998;
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02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ,
                                                                  20-SEP-1999
                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999.
                                                                                                                                                        diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCCOY JM,
                                  AAY06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.
                                                                                                                                                                                                                                       Peptide
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contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polynucleolide that comprises treating a test sample with at least one LS170-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LS170 gene. The LS170 which are fragments represent a set of configuous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease. Particularly detection of LS170 polynuclectide, LS170 antigens, or anti-LS170 antidodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used to isolate related sequences; as standards and reagents in sasays, as targets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or triplex-forming agents, ho can be used to deliver therapeutic agents to LS170-expressing cells; directly as therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170-related nucleic acid
                  144 PTSISLSLLDKHSQ1-INKFVNSVINTLKSTVSSLLQKEICPLIKIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAW95463-471 represent LS170 polypeptide fragments which
                                                                                                                                                                                                                                                                                                                                                                        LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New LS170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Cohen M, Colpitts TL, Friedman PN;
dosen, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US11601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0049183,
                                                                                                                                                                                                                                                                                             29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                   LS170 polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billing-medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 AA;
                                                                             203 DNPQHKTQ 210
                                                                                                                244 nmlihglq 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX00809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1998.
                                                                                                                                                                                                                                                        AAW95463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                               AAW95463
                                                                                                                                                                             RESULT
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Lung specific genes for developing products for diagnosing, monitoring,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is encoded by a lung specific gene, designated Lug110, clone ID 135520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating luny cencer, especially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for
                                                                                                                                              85 DCKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                             144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                     65 IgilenlpildilkpgggtsggllggllgkvtsvipgInniidikvtdpqllelglvqsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                     28 IGVLQKSSAWQLAKQKAQEAEKILLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8%; Score 178; DB 21; Length 256; 24.5%; Pred. No. 7.5e-09; tive 44; Mismatches 92; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    staging, prognosticating, imaging and treating lung cancer
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of lung specific protein Lng110.
Best Local Similarity 24.5%; Pred. No. 7.5e-09;
Matches 46; Conservative 44; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sun Y, Recipon H, Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 35-36; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             AAY69164 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US16247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0095233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DIAD-) DIADEXUS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 45; Conserva:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA;
                                                                                                                                                                                                                                                                     203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                                                    244 nmlihglq 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200008206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY69164;
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                                                                                                                                                                                                                                                                                                                                                                            AAX69164
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16.8%; Score 178; DB 20; Length 256;

Query Match

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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cyll proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; antiinflammatory; immunosuppressive; noutcorotective; antiarthritic; autimicrobial; vulnerary; orgotestic; antidiabetic; virucide; antiinferrility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antiparkinsonian; immunostimulant; dermatological; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; oytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis, graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                125 dghrlyvtiplgiklgvntplvqasllrlavklditaeilavrdkgerihl-vlgdcths 183
                                                                                                                                                                                                                                                        144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                        85 DGKGLNLSFPVTANVTVAGPIIG-QIINFKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lavallie E, Collins-racie LA,
J, Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 497-498; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU39019 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001; 2001WO-US09369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2000; 2000US-0729674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food supplement; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K, McCoy JM, La
Treacy M, Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark H, Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639363/73.
                                                                                                                                                                                                                                                                                                                                                                                                                203 DNPQHKTQ 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU39019;
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AAU39019
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Search completed: August 6, 2002, 16:52:52

Job time: 334 sec

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systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-lost diseases (CVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system,
                                                                                                                                                                                                                                                                                   sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 DCKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
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                                                                                                                                                                                                    Alzheimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 I.GVI.QKSSAWQLAKQKAQEAEKLLNNVISK---LI.PTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%; Score 178; DB 22; 24.5%; Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Conservative
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Best Local Similarity
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Run on:

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APPLICANT: Heinen, Erns
TITLE OF INVENTION: PAR
TITLE OF INVENTION: PRE
TITLE OF INVENTION: SYN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
Z1P: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-700-548-4
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Query Match
(without alignments)
102.528 Million cell updates/sec
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Sequence 6, Appli
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Agreemence 2, Agreemence 98, Asequence 98, As
                                                                                                                                                                                                                                      1 KLEPVLHEGLETVDNTLKGI........nvIQQVVDNPQHKTQLQTLI 215
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Sequence 98,
Sequence 6, A
Sequence 2, A
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Sequence 51
Sequence 12
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                                                                                                                         August 6, 2002, 16:53:52; Search time 51.22 Seconds
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2: /cgn2_6/ptodate/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodate/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodate/2/iaa/6E_COMB.pep:*
5: /cgn2_6/ptodate/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodate/2/iaa/pcTUS_COMB.pep:*
             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08 480-604A-6
US-08 460-604A-6
US-08 405-136-4
US-08 -915-136-4
US-08 -915-136-4
US-08 -916-136-4
US-08 -916-238-4
US-08 -912-2
US-08 -910-912-2
US-08 -910-912-2
US-08 -912-2
US-08 -913-7
US-08 -912-2
US-08 -913-7
US-08 -913-7
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US-08 -913-7
US-08 -913-7
US-08 -913-7
US-08 -916-98
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                   US-10-020-139-2_COPY_35_249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Score Match Length DB
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Perfect score:
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                                                                                       OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98,
Sequence 4,
Sequence 4,
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Sequence 2,
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Sequence
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Pred. No. 0.23;
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US-08-485-445A-98
US-08-779-400-2
US-08-55-660-2
US-09-119-263-98
US-09-23-480-98
US-09-23-5480-98
US-09-35-53-99
US-09-35-5480-2
US-09-35-545-2
PCT-US94-02465-98
PCT-US94-06931-4
PCT-US95-00656-98
US-08-431-4
US-08-785-431-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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OPERATING SYSTEM: System 7.5
SOFTEM: Apple Macintosh 6500
OPERATING SYSTEM: System 7.5
SOFTEM: MordPerfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,548
FILING DATE: 30-AuG-1996
CLASSIFFCATION DATA:
APPLICATION NUMBER: PCT/FEP95/00642
FILING DATE: 22-FEB 1995
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: DE 44 07 489.1
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: DE AT 07 ARPLICATION DATA:
APPLICATION NUMBER: DE AT 07 ARPLICATION NUMBER: APPLICATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/08700548; Patent No. 5910310; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33.141
REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHERACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8%;
26.2%;
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amino acid
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99; Indels 52; Gaps
                                                                                 80 LOPI-GENLETIRNOLIPTRRRRFACVVICLAA-LGVATAAQVTAAVALVKANKNAAAI 137
                                                                                                                             50 I.-LUNVISKLIPTNTDIFCLKISNSLILDVKAEPIDUGKGLNLSFPVT-ANVTVAGPIIG 107
                                                                                                                                                                       138 LNI,KNAIQK---TNTAVADV-VQATQSI,GTAVQAVQDHINSVVSPAITAANCKAQDAIIG 193
                                                                                                                                                                                                               108 QIINLKASLDILTAVTIETDPQTHQPVAVLGECASDPTSIS---LSLLDKHSQIINKFVN 164
                                                                                                                                                                                                                                                                                                       165 SVINTLKSTVSSLLQKELCPL-----IRIFIHSLDVNVIQQVVD------NPQH 207
                                                                                                                                                                                                                                                                                                                              2 LEPVLHEGLETVDNTL-----KGILEKLKVDLGV---LQKSSAWQLAKQKAQEAEK 49
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APPLICANT: THAILEY, BRUCE S.
APPLICANT: THAILEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TRHAFMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: MEDILEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMHER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
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02-DEC-1993
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08480604A Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-1992
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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APPLICANT: KINK, J
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1012 LISNAVNDTINVEPTITEGI-----PIVSTILDGINLGAAIKELLDEHDPLLKKELEAK 1065
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                                                                                                                                                                                                                                                                                                                                                                    98; Indels 42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLEPVLHEGLETVDNTLK--GILEKLKVDLGVLQK------SSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 LLN--NVISKI,LPTNTDIFG------LKISNSL,ILDVKAEPIDDGKGLNLSFPVTA 97
                                                                                                                                                                                                                                                                                                                   Nucry Match 8.6%; Score 91; DB 1; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8; Matches 50; Conservative 51; Mismatches 98; Indels 4
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TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: 220 MONTGOMERY STREET, SULTE 2200
REFERENCE/DOCKET NUMBER: OPHU-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/405,496A
16-MAR-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161 007
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/08405496A; Patent No. 5919665; GENERAL INFORMATION:
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEGOERICE CHARACTERISTICS:
LENGTH: 2710 amino acids
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                                                                                                                                                                                   TOPOLUGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: SAN FRANCISCO
STATE: CALIFORNIA
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                                                                                                                                                                    TYPE: amino acid
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959 NTLNAAFFIQSLIDYSSNKDVLNDLSTSVKVQLY---AQLFSTGLNTIYDSIQLVN---- 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLEPVLHEGLETVDNTLK--GILEKLKVDLGVLQK-----SSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 LLN--NVISKLLPTNTDIFG------LKISNSLILDVKAEPIDDGKGLNLSFPVTA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%; Score 91; DB 2; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8; Matches 50; Conservative 51; Mismatches 98; Indels A
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STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                             ATJUNEAL DOLLA, DIANE E.
REGISTRATION NUMBER: 40,027
REFRENCE/COCKET NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 397-838
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
Arplication NUMBER: US 07/429,791 FILING DATE: 31-0CT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-405-496A-6
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                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-915-136-6
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158 IINKFVNSVINTLKSTVSSLLOKEICPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTL 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.6%; Score 91; DB 4; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8; Matches 50; Conservative 51; Mismatches 98; Indels 4
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APPLICANT: Piets, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MATKET SCHWARZE JACOBS CONTEST: 1601 MATKET STREET: 3611 MATKET STREET: 1601 MATKET STREET: 3611 MATKET STREET
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/329,154
PRIOR PAPLICATION DATE: 25-CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-CCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
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US-08-790-912-4
: Sequence 4 Application US/08790912
: Patent No. 5976542
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-136-6
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                                                      FILING DATE:
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CITY: Ph
STATE: P
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E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 KEQSLAAESKTVLQELINVLKTDLLSSLEMILSPTV---VSILKIN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27129/32137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Sequence 49, Application US/08261660A
. Patent No. 5731415
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312/474-6300
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
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Illinois
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Best Local Similarity 23.0%; Pred. No. 1.6;
Matches 52; Conservative 35; Mismatches 79; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 -----KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTA-V 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          794 KADNSKISNSSF------KGRIVN-SYETKAPYNIGG-LVGQLTGINALVDKSKATI 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743 TVENLTLKDVNISGKTDIGAL-----ANEANNATRINNVHVDGVLAGERGIGGLVW 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.5%; Score 90.5; DB 2; Length 1861; Best Local Similarity 26.5%; Pred. No. 2.5; Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 TIETD-PQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLK 171
                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/790,912
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CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: Sakowicz, Roman
APPLICANT: Bakowicz, Roman
TITLE OF INVENTION:
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                                                                          FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION IMPA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFREENCE/DOCKET NUMBER: 7600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2991
TELEFAX: (215) 567-2991
                                                                                                              COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MC-SOFEM: PC-DOS/MC-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEO ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1861 amino acids
                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-790-912-4
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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US-09-541-782-10
                              19103-2398
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US-09-541-782-10
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COUNTRY:
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506 TTKDVSCLHSKLDRKKAVDQHINAEAQDIFGKNLNSLFINNMEELIKDGSSKQKAMLEVHKT 565
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                                                                                                                                                                                                                                                                                                                                                              566 LFGNLLSSSVSALDTITTV------ALGSLTSIPENVSTHV----SOIFNMIL 608
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10 LETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQK----AQEAEKLLNNVISKLL----P 60
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APPLICANT: Ruben, Steven M.
APPLICANT: Sonenberg, Nahum
APPLICANT: Sonenberg, Nathalie
APPLICANT: Methot, Nathalie
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APPLICANT: Methot, Nathalie
APPLICANT: Methot, Nathalie
APPLICANT: Rom, Eran
TITLE OF INVENTION: (as amended)
TITLE OF INVENTION: (as amended)
TITLE OF INVENTION: (as amended)
CURRENT APPLICATION NUMBER: US/09/546,238
CURRENT FILING DATE: 2000-04-10
CORRENT FILING DATE: US 66/033,151
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TITLE OF INVENTION: ETHGF-like Protein (p97) Genes FILE REPERENCE: 1480-0700001

CURRENT APPLICATION NUMBER: US/08/990,140A

CURRENT FILING DATE: 1997-12-12

EARLIER APPLICATION NUMBER: US 60/033,151

EARLIER FILING DATE: 1996-12-13

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1
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143 DPTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV 195
                                                                                           138 DIADVEVDMSGDLGWLLNLFHNQIESKFOKVLESRICEMIQKSVSSDLQPYLQTLPV 194
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. Patent No. 6316225
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APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
TITLE OF INVENTION: Use of said Genes and Proteins
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUBBER: US/08/810,712G
CURRENT FILING DATE: 1997-03-03
EARLIER APPLICATION NUBBER: PCT/US94/11598
EARLIER TILING DATE: 1994-10-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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Patent No. 6160106
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 907
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ORGANISM: Homo sapiens
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1004 WDRTSGEEKHAGE-LINVLSDVNVINGNAITGYHYTGMKVANTFSSKANRVFNVTLE--K 1060
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                                            791 ISPKLHVDKGFVNILMTSFLOYISSEVNPPSDETDSSSAPSKEQLEQEKQLLLSFKFVMQ 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.9%; Score 83.5; DB 2; Length 1964; Best Local Similarity 24.3%; Pred. No. 14; Matches 49; Conservative 34; Mismatches 68; Indels 51;
                                                                                                                                                                                                                                                                                                                    APPLICANT: Weiser, Jeffrey N.
PADLICANT: Plant, Andrew TITLE OF INVENTION: OF STREPTCCCUS PNEUMONIAE INFECTION
TITLE OF INVENTION: OF STREPTCCCCUS PNEUMONIAE INFECTION
                                                                                        161 KFVNSVINTLKSTVSSLLQKEI-C-----PLIRIFIHSLDVNVIQQ 200
                                                                                                                 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREFT: 1601 Market Street, 36th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/790,912
FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 7600-401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEO ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMHER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 Sequence 3, Application US/08790912
Patent No. 5976542
GENERAL INFORMATION:
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IBM PC compatible
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REGISTRATION NUMBER: 36,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennsylvania
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ZIP: 19103-2398
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US-08-790-912-3
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1077 WDRTSGEEKHAGE-LINVLSDVNVTNGNAITGYHYTGMKVANIFSSKANRVFNVTLE--K 1133
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                                                                                             APPLICANT: Weiser, Jeffrey N.
PAPLICANT: Plaut, Andrew G.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
                                                                                                                                                                                                                                              ADDRESSEE: PANITCH SCHWAKZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/790,912
FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                         ; Sequence 2, Application US/08790912
; Patent No. 5976542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
TELEPHONE: (215) 567-2020
TELEPHAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 2:
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REGISTRATION NUMBER: 36,317
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                             NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       Pennsylvania
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                                                                      GENERAL INFORMATION:
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US-08-431-517F-2
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
US-08-790-912-2
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Chicago
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US-08-261-660A-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIINLKASLDL-LT 120
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                                                                                                                                     APPLICANT: Scott, Randal W
APPLICANT: Scott, Randal W
APPLICANT: Marra, Marian N
TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS
FILE REFERENCE: 1103/11307Us01
CURRENT APPLICATION NUMBER: US/08/431,517F
CURRENT ETLING DATE: 1995-05-01
NUMBER OF SEQ ID NUS: 17
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
CORRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 STVSSLLQKEICPLIRIFIHSLDV------NVIQQVVDNPQHKTQL 211
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
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REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECHOMATICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
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Sequence 2, Application US/08431517F Patent No. 6265187 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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ORGANISM: human
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LENGTH: 481
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85 --- DGKGLNLSFPVTAN----VTVAGPIIGQIINLKASLD------LLTAVTIETDPQ 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 THQ-------PVAV-----LGECASDPTSISLSLLDKHSQIINKFVNSVINTLK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 LQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD-----VKAEP1D- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 IQEAVADYLXIELKEKTKSARADMLRKMLVAKSD--GGKNKFLVILDDVWQFVDLEDIGL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Lipopolysaccharide Binding Protein Derivatives NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 STVSSLLQKEICPLIRIFIHSLDV------NVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 DYLODQETKYIFLLCGLFPEDYNIPPEELMRYGWGLNLFKKVYTIREARARLNTCI 235
                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 20.8%; Pred. No. 2.9;
49; Conservative 42; Mismatches 90; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Scars Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                    LOCATION: 1..468
OTHER INFORMATION: /nole- "RG2P deduced sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,660A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 27129/32137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 51, Application US/08261660A
; Patent No. 5731415
; GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acids
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NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,8
                 SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
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312/474-0448
INFORMATION FOR SEQ ID NO:
                                                                                                                                                          protein
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Best Local Similarity
                                                                                                                                      linear
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-660A-51
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9 Query Match
7.6%; Score 81; DB 1; Length 197;
Best Local Similarity 19.4%; Pred. No. 0.92;
Matches 28; Conservative 38; Mismatches 64; Indels 14; Gaps 64 DIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQ--JINLKASLDL-LT 120 52 EPHSLNIHSCELLHSALRPV-PGQGLSLSIS-DSSIRVSGKWKAQKRFLKMQGGFDVSVK 109 qq

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172 STVSSLLQKEICPLIRIFIHSLDV 195 δ

Search completed: August 6, 2002, 16:53:54 Job time: 286 sec

Run on:

Title:

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MB3210 Rattus norv
M26806 Mouse parot
AE001165 Deinococc
AF423315 Homo sapi
E53840 LUNX gene a
AF172993 Homo sapi
E53841 LUNX gene a
AB024937 Homo sapi
BC012549 Homo sapi
AF158745 Homo sapi
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b43949 Human mRNA
AX123429 Sequence
AX066081 Sequence
AC107180 Rattus no
AL13090 Human DNA
AC021774 Homo sapi
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ACO95073 Rattus no
ACO94951 Rattus no
AC107726 Mus muscu
                             U79413 Bos taurus
U79414 Bos taurus
BC010288 Mus muscu
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Homo sapi
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Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1058)
Mumas millen Edwards,J.B., Bouqueleret,L. and Johert.S.
Complementary dna S encoding proteins With signal peptides
Patent: WO 0100806-A 26 04-JAN-2001;
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AX224647 Sequence
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                                                                            AL121901 Human DNA
                                                                                             X01697 Mouse mRNA
                                                                                                                          X68699 M.musculus
AX061621 Seguence
AF432917 Homo sapi
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AL445327
AC005411
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AC090376
AP001497
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/note="unnamed protein product"
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Sequence 26 from Patent WO0100806.
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/db_xref="taxon:9606"
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AB024937
BC012549
AF158745
MUSPSPA3
                                              BTU79414
BC010288
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AE001965
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AC021774
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18.6 161593
18.6 867
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746.8
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190.6
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AX061621
LOCUS
DEFINITION
ACCESSION
VERSION
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ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
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                                                                                                           Claims 1 d. 2
                                                                                                      August 6, 2002, 16:01:08 ; Search time i816.11 Seconds (without alignments) 11845.362 Million cell updates/sec
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                                                                                                                                                                                                     1 CACGAGATTTCATGAGCATC......AAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                  1797656 segs, 10463268293 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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em_htg_hum:*
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Maximum DB seq length: 200000000
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Match Length DB
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ETVDNTLKGILEKLKVDLGVLQKSSAMOLAKQKAQEAEKLLNNVISKLEPTNTDIFGL
KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIET
DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRIFIHSLDVNVIQQVVDNPQHKTQLQTL!"
                     /translation="MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
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                                                                                                   /note="Von Heijne matrix score 5.20 seq QLWKLVLLCGVLT/GT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.2%; Score 1019.8; DB 6; Length 1058; 99.8%; Pred. No. 4.4e-267;
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/protein_id="CAC24982.1"
/db_xref-"G1:12406704"
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302 c
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PRI 07-NOV-2001
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ETVDNTLKGILEKLKVDLGVLOKSSAWQLAKQKAQEAEKLLNNVISKLLPTNYDIFGL
KISNSLILDVRAEPIDOKGKLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIET
DPQTHQPVAVLRECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRIFIHSLDVNVIQQVVDNPQHKTQLQFLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (benkatesh, S. G., Geetha, C. and Gorr, S. -U. A member of the PSP/ptunc family of BPI proteins is expressed in the human parotid gland
                                                                                                                                                                                966 CAGAACAGCAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                                                                                                                                                                                    804 AACCCTCATCTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 863
                                  846 AGTGGCTTGCCCCACCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAAC 905
                                                        906 CAGCGIGAAAGCCIGAGICCCACACAGAAGGACCIICCCAGAIACCCCIICICCICACAGI 965
                                                                                                                            49 ATGCTICAGCTTTGGAAACTTGTTCTCCTGTGCGGGGTGCTCACTGGGACCTCAGAGTCT 108
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Venkatesh, S.G. and Gorr, S.-U.
Direct Submission
Submitted (12-OCT-2001) Molecular, Cellular and Craniofacial
Biology, University of Louisville, 501 S. Preston Street,
Louisville, KY 40292, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 CTICTIGACAAICITGGCAAIGACCIAAGCAAIGTCGIGGAIAAGCIGGAACCIGITCII 168
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similar to BSP30 and plunc/lunx"
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/db_xref="G1:16755850"
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/chromosome="20"
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BTU79413 999 bp mkNA linear MAM 09-DEC-1996
Bos taurus common salivary protein BSP30 mkNA, form a, complete
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The clouds and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                           121 CACCAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTC
                                                                                                                           GCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTT
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                                                                                                          GACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAA
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Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
Direct Submission
Submitted (21-NOV-1996) Dairy Science Grou
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 ATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCA 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 TGTTGGGTGAGATTGTCAAACTGGACCTCAATGTGGACCTCCAAACTAGTGTCAGCATTG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              667 GAATCCGTGAACTCCTTGAAAGCCTGGATACAGAGTGTATTAAGAAACTCATTGGTGAAC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 AATCTCTTCTTGACATTCGTGGCAA-----CGATGTTCTGAGGAGGCTGATATCTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TTACAGGGGTGAGAATCAGGAACGTCCAGGTCCCGGATATCACATTCGAAGCGA---CTT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTG 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 35; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.1%; Score 237.4; DB 4; Length 999; Best Local Similarity 57.3%; Pred. No. 9.8e-54; Matches 564; Conservative 0; Mismatches 386; Indels 35.
                                                                                                                                                                                  /note="common salivary protein, form a"
                                                                             /tissue_type="parotid gland"
36. .767
/organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                         /product-"BSP30"
                                                                                                                                                                                                                                  /codon_start=1
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MAM 09-DEC-1996
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DITFEATSENSANVLIPITADVTVSLPFLGEIVDLDLAVDLOTTVSIETDTEDPOVVV
GECTINPESISLIVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MVQLWKLVLLCGLLAGTSAS;PDIRGNDVLRKLKSGLERGLDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
The cloning and sequencing of two cDNAs coding for alternate forms
of BSP30, a bovine member of the Parotid Secretory Protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammanlai Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bos. 1 to 1024)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1024)
Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
Direct Submission
Submitted (21-NOV-1996) Dairy Science Group, AgResearch, Private
                                                                                                                                                                        944 AGATACCCCTTCTCCTCACAGTCAGAACAGCCTCTACACATGTTGTCCTGCCCCTGG 1003
                                                                                                                                                                                                                                                                                                                                                                                                                  BTU79414 1024 bp mRNA linear MAM 09-DEC-1
Bos taurus common salivary protein BSP30 mRNA, form b, complete
787 GCCTGCTGACTGCTTCCAGGACGTGACTGAATCTCTGTACCGTCT---TCCTCTGGGGACG 843
                                                                                      884 GAAGCIGCIGCCACCACCTAACCAGGGTGAAAGCCTGAGTCCCACCAGAAGGACCTICCC 943
                                                                                                                844 GTCGGTGCTGCCACCACCACCAGGAGGACACTCAAAGGACACTCTCAC 903
                                                                                                                                                                                                904 A----CACTCGTCGTCACAGTCAGGA---CACCCTATGCTTGTCACCCCCCCACCCCCAG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 AGTCTTTTTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 AAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAG 103
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56.9%; Pred. No. 7.9e-49;
tive 0; Mismatches 381;
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/db_xref="G1:1710369"
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/db_xref="taxon;9913"
                                                                                                                                                                                                                                                               1004 CAATAAAGGCCCATTTCTGCAAAAA 1028
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974 bp mRNA linear ROD 29-OCT-2001
IMAGE:2616413, mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                      141 GICTIGAGAGAGACTIGACACTITGACAGIACAATIGAAATITGAGAATITGA 200
                                                                                                           201 AGACTGAATT------GGAATCCAGGTGTTCAGACGAGGTTGTGAGACA---AC 245
164 TICTICACGAGGGACTIGAGACAGITGACAATACTCTIAAAGGCATCCTIGAGAAACTGA 223
                                                                                224 AGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAGGCCC 283
                                                                                                                                                                284 AGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACA 343
                                                                                                                                                                                                        246 AGGAAACTGAGAATTTCTTGGAACAACTCATTTCTAGAATTTTTCAAGTAGTGAGCAGGC 305
                                                                                                                                                                                                                                                 306 TTACAGGGGTGAGAATCAGGAACGTCCAGGTCCCGGATATCACATTCGAAGCGA---CTT 362
                                                                                                                                                                                                                                                                                                                                   404 ATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGCAATGTCACTGTGGCCGGGCCCA 463
                                                                                                                                                                                                                                                                                                                                                              464 TCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 CCAGCATCTCACTTTCCTTGCTGGACAAACACGCCAAATCATCAACAAGTTCGTGAATA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 GCGIGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCAC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 TIGGAGICAACCTIGCGAGAAGGIGGIGICCICIGIAGIGGAGGGCGAGCIGIGCCCAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 TGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 GATICCGCGAGCICCTIGAAAGCCIGGAIGCAGAGIGITIGAGAAACICATIGGCGAGI 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 CTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAG----- 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 CTCAGGACCACCAACAGGAACCTGAAGGCAGCAGGATGAGGAAACCGCTGGGATGCCC 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        876 CCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837 CTCTIGGGACAGGCGGTGCTGCCACCATCCCCCAGGAATGACAACTGAGCCCAGTCAAAGG 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 897 ACACTCTCGGATACTCATGCTC --- - ATAGTCAGGACACCCTATGCTCATCACCTCC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 AAACTGATCCCCAGACACACCCGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 GACCACTGTGGTGCATGCTTGGTTCCCAGTGGCTTGCCCCACCCCTTATAGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         996 GCCCTGGCAATAAAGGCCCATTTCTGCAAAA 1028
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 16 Row: g Column: 1.
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LSSNGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGK
CSSNTDKISISLLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Lissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFQLGSLVVLCGLLIGNSESLLGELGSAVNNLKILNPPSEAVPQ
                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Center: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
Villalon, D.K., Luna, B.A., Hale, B.Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
                                                         Direct Submission
Submitted (05-JUL-2001) National Institutes of Health, Mammalian
                                                                                                               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ------AAATTCTGAATCCTCCTCTGAAGCTGTCCTCAGAAC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
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                                                                                                                                                                                                                                                                                              Tissue Procurement: Jeffrey Green M.D.
CDA Library Preparation: Life Technologies, Inc.
CDA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="parotid secretory protein"
/protein_id="AAH10288.1"
/db_xref="G1:16307481"
                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 198; DB 10;
Pred. No. 5.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:11605 IMAGE:2616413"
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45. 752
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/lab_host="DH10B"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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(bases 1 to 974)
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nes 511; Conservative
                               Strausberg, R.
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                                                                                                                                                                                                                                           COMMENT
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HSBA49G10
HUMBA DNA linear PRI 20-JUN-2001
HUMBA DNA sequence from clone RPI1-49G10 on chromosome 20 Contains a gene similar to bovine salivary protein BSP30, the LOC51297 gene for LUNX protein, 5, end of a gene encoding a protein similar to secundogene minor salivary gland protein, a novel gene, a pseudogene similar to STAT-induced STAT inhibitor-2, a pseudogene similar to ribosomal protein L12, a putative novel transcript, AL121901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 5, 2000 this sequence version replaced 91:8017404.
                                                                                                                                                                                                                                                                                         657 CCATIGCTICAGIACGICCICAGCACACIGAAICCAAGIGIICIICAGGGICICCICTCI 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   717 AATCTACTG --- GCAGGACAGGTACAACTTGCCCTCTGAAGAGGAAGAACAGAAGGATGC 773
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340 GACATITITIGGGTIGAAAATCAGCAACTCCCTCATCCTGGAIGTCAAAGCTGAACCGATC 399
                                                               297 AATGGTTTATTGTTGAAAATCAATAATGTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 356
                                                                                                                            400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                        357 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
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                                                                                                                                                                                                                                                                                                                                                                                520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 GATGGTGTCTTACCTCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTCCTATGT
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1 (bases 1 to 161593)
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18333. .18770
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                                                           complement (20975
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; BMEL: Swi. SWISSPROT: Tr.; TREMBL: Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP1149G10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP1149G10 is at 1 in this sequence. The true left end of clone RP511874 is at 164494 in this sequence. The true right end of clone RP511874 is at 164494 in this sequence. The receipt as clone RP4-73302 is at 27823 in this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI1+2/Www.chori.org/bacpac/home.htm

VECTOR: PARCES 16
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14772. .14779
/note="randem repeat. Forced join. Approximately 500 bases 16219. .16387
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5184. .5344
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/note="match: 6104. .6463)
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complement(14766. .15061)
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/note="2 co
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LIRIFIHSLDVNVIQQVVDNPQHKTQLQTI"
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BSP30)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="bA49G10.1 (similar to bovine salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LiPA8 repeat: matches 4514, .5125 of consensus" 38750, .39785
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61. .705
                                                                                                                                                                                                                                                          /product="put. PSP (parotid secretory protein).(aa 1-215)"
227 c 168 g 252 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 AAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 GGCAAGACGCTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCCCATTAAAACC 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529 GATCCCCAGACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 ATCTCACTITCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 ATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       709 CGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                769 CACAAAACCCAGCTGCAAACCCTCATTTGAAGAGAGGAATGAGGAGGACGACTGTGGGTG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 190.6; DB 10; Length 867;
55.3%; Pred. No. 5.6e-41;
Live 0; Mismatches 359; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AIGCTICAGCTTTGGAAACTIGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 CTICITGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 CACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAGGCCCAGGAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGCATTCTAGAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 ACGITGAACACAGCGGACCITGGCAAITTAAAAAGCTITACAICTTIGAAIGGTITAII- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 AATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAATACAGATAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 TCTACCCTCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTCCTATGTCCATTGCTT 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"PSP"
/protein_id-"CAA25846.1"
/db_xref-"GI:758163"
                   /codon_start*1
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Matches 503; Conservative
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1 (bases 1 to 867)
Madsen, H.O. and Hjorth, J.P.
Molecular cloning of mouse PSP mRNA
Nucleic Acids Res. 13 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                match: proteins: Tr:095102 Tr:088582 Tr:014542 Tr:014509
Tr:062225 Tr:015097 Tr:035718 Tr:090x77 Tr:090x78
Tr:070512 Tr:035960 Tr:09PW70 Tr:09Y5R1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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95.2%; Pred. No. 6.8e-41;
iive 0; Mismatches 10; Indels 0; Gaps
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/note="bA49G10.2 (similar to STAT-induced STAT
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53972. .54142
/note="match: GSS: Em:AQ429347"
54000. .54141
/note="match: GSS: Em:AQ392510"
complement(54027. .54139)
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                   /note="match: GSS: Em:AF101963"
53858 . 5402
/note="match: GSS: Em:AQ392891"
complement(53908 . 54141)
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54030. .54138
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53970, .54139
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54041, .54149
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53958. .54139
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complement(53844. .54141)
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54767, 54660
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/trānslation="MPQLGSLVVLCGLLIGTSESLLGDVANAVNLDILNSPSEAVAO MNLDDVGSLOQATTWPSAKDSILETLHKVELGNSVGFPLDLGLLLRVRFRVLDLGAG LSSNGKDIDLKLPVFEISTSLPVIGPTLDVAVSLDLLNSVSVQTNAQTGLFGVTLGK CSGNTDKISISLLGRRLPFVNRILDGVSGLLTGAVSILLQNILCPPLLQVLLSTNSGSA
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Neonatal rat submandibular gland protein SNG-A and parotid
secretory protein are alternatively regulated members of a salivary
protein multigene family
J. Biol. Chem. 267, 2679-2687 (1992)
                                                                                                                                                                                                                                                                                                                       RATPSP 962 bp mRNA linear ROD 24-MAR-1998 Rattus norvegicus neonatal submandibular gland protein precursor
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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California, 401 Barker Hall #3204, Berkeley, CA 94720-3204, USA
                                                                                                       889 TGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCACCAGAAGGACCTTCCCAGATA 948
739 CCTGCTGGCTACTCTCCAGTGGTTTCATCTTACTTCTGATGGCATTTCCCTCTAGAAAG- 797
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/Lissue_type="submandibular gland"
/dev_stage="neonatal"
1..962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC06334.1"
/db_xref="G1:206457"
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/db_xref="taxon:10116"
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/note="secreted form"
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Rattus norvegicus
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180 ATCTGAATCTGGATGTGGGGTCACTTCAGCAAGCCACAACTTGGCCATCAGCCAAGGACA 239
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                                                                                                                                                                                                                                                                                                                                                                      158 AACCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGA 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AACTGAAGGICGACCTAGGAGIGCTICAGAAATCCAGIGCTIGGCAACTGGCCAAGCAGA 277
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                                                                                                                                                                                                                                                                              98 CCTCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGG 157
                                                                                                                                                                                                              36 CCAAACCAAAGATGTTCCAACTTGGGAGCCTTGTGGGTCTTGTGGGGA 95
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                                                                                                              3.1e-36;
                                                                                          16.8%; Score 173.2;
53.1%; Pred. No. 3.1e
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                                                                                                                                         Matches 490; Conservative
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Mirels, L. and Ball, W.D. Webailal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein multigene family
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7756 GACCTCATAAATTCACTCTCCATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACC 7815
                                                                                                                                                                                                                                                                                                                                                                                         439 GCGAATGTCACTGTGGCCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTG 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATSMGB 827 bp mRNA linear ROD 07-API Rattus norvegicus neonatal submandibular gland proacinar cell protein precursor (SMGB1/SMGB2) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                          6.9%; Score 70.6; DB 10; Length 13962; 60.8%; Pred. No. 3.7e-08; Live 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                  3 others
                /product-"parotid secretory protein"
11287. .11361
/gene-"Psp"
                                                                                                                                                                                                            /product="parotid secretory protein" 3075 c 3231 g 3930 t 3 o
                                                                                                             /product="parolid secretory protein"
12262. .12433
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                      /note="exon h"
                                                                                                                                                  /gene="Psp"
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/number-7
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Rattus norvegicus
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Direct Submission
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Svendsen, P., Laursen, J., Krogh-Pedersen, H. and Hjorth, J.P. Novel salivary gland specific binding elements located in the PSP proximal enhancer core
Nucleic acids research. 26 (11), 2761-2770 (1998)
                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 13962)
Mikelsen,T.R.
Direct Submission
Submitted (07-0CT-1992) T.R. Mikkelsen, Department of Molecular
Biology, University of Aarhus, CF Mollers Alle 130, 8000 Aarhus,
DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /germline
//clone_lib-"Lambda-PHAGE (Lambda L47.1)"
/clone="Lambda YP1, Lambda YP3, Lambda YP7"
/map-"Estimate: 69 cM from centromere"
/note="Allele: b"
                        MMPSPG 13962 bp DNA linear
M.musculus Psp gene for parotid secretory protein.
X68699
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/product="parotid secretory protein"
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10779. .10842
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/note="exon g"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="2"
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/evidence-experimental
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parotid secretory protein.
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/gene="Psp"
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/yene="Psp"
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/gene="Psp"
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AHDIJTDVSISMEATTSFATEKDPKTGRRVLMMQRCSLNTDNTSISLLNRKSNEVNLA
LDSALYLIKRGLTLPVRRQLCPVLQLIISNTFHPDEISNPQTAISI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 bp DNA linear ROD 20-MAY-1994 boxone parotid secretory protein (PSP) gene, exon 2, clone YPLE2.8. M26806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 TCGAGITGAAAATCAAGGACCTCAGAATTCTGAACCTGAATCATGAAGTGTCTCCCAATG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 GIGATITAACTACTGATGICTCTATTICTATGGAGGCAATAACTTCCTTTGCTATTGAAA 394
                                                                                                                                                                                                            /product-"neonatal submandibular gland proacinar cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="neonatal submandibular gland proacinar cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 GCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGGAATGTCACTGTGGCCGGGCCCATCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 ITGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 CTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AAGATCCCAAGACTGGCGTCGTGTCCTGAACATGCAGCGATGCTCACTTAATACAGACA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 ATACCTCCATTAGCTTGTTGAACAGAAAAGTAACTTTGTCAACTTAGCTCTGGACTCTG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 IGAICAACACGCIGAAAAGCACIGIATCCICCCIGCIGCAGAAGGAGAAIAIGICCACIGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                     /qene="SMGB1/SMGB2"
/note-"parotid gland protein SMGB; sublingual gland
protein SMGB; differently N-glycosylated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 GCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 6.3%; Score 65.2; DB 10; Length 827; al Similarity 48.4%; Pred. No. 8.7e-07; l81; Conservative 0; Mismatches 193; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parotid secretory protein; secretory protein. 2 \text{ of } 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (strain C3H.Amy-YBR) spleen DNA.
/Lissue_type="submandibular gland"
/dev_stage="neonatal"
1. .827
                                                                                                                                                                                                                              Protein precursor"
/protein_id="AAC12783.1"
/db_xref="G1:206990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /yene="SMGB1/SMGB2"
206 c 160 q
                                                                 "SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                                     "SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 g
                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M26806.1 GI:200555
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811. .81
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                                                                                                                                                                                                                                                                                                                                                                                                     /gene-
85. .64
                                                                   /dene*
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Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 210)
Poulsen,K., Jakobsen,B.K., Mikkelsen,B.M., Harmark,K., Nielsen,J.T. and Hjorth,J.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Fraser, C.M. et al. Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 12334)
White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D.,
Dodson,R.J., Haft,D.H., Grinn,M.L., Nelson,W.C., Richardson,D.L.,
Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby.M., Shen,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordination of murine parotid secretory protein and salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 TGTCAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTG 94
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Deinococcus radiodurans R1 section 102 of 229 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.1%; Score 62.6; DB 10; Length 210; Best Local Similarity 73.4%; Pred. No. 3.9e-06; Matches 80; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 GGACCTCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Psp"
/note="first expressed exon"
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                                                                                                                                                                                                                                                            /organism~"Mus musculus"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/map="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 g
                                                                                                                                                                                                                                                                                                                                                /tissue_type="spleen"
                                                                                                                                                                                                                                                                               /strain="C3H.Amy-YBR
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                    amylase expression
EMBO J. 5, 1891-1896 (1986)
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185. .>210
/gene="Psp"
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AE001965.1 G1:64
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Mus musculus
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                                                                REFERENCE
                                                                                   AUTHORS
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MEDLINE
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                                                                                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
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/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to 1018/05/293 percent identity: 62.08; identified by sequence similarity; putative, hydroxypyruvate reductase, putative, authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTRTPLTLEQLNALSDDAFTEHFAGVLEHSPHYARRAAAGRPFA
DVEEVAAAFARAVAADEPGAQVQLIRAHPDLAGKAALAGELTAESASEQTSAGLDRLS
PEEYAEFQRLNAAYHERFGLPYVVCVRENTKDTIFEGARRRLTHTQEEEQAAALHEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKAGLSASTTYRLLETLRQQGYVEWEERSGLFSVGLRAYQVGAAFSERNSLLSAAGA
VMQALVEEVNETANLAVLRGNEAVYVHQVEASQLMRMETHIGAAAPLHCSGVGKVLTA
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TSNRIVRLLEKGLIERREDERDRRSASIRLTPQGRALVTHLLPAHLATTQRVLAPLSA
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AKVRVAMYGDFGAAHSEGDNTDLVATDTVRNTVYGLAKEGFESSIEEFGKELLTHFVK
                                                                                                                                                                                                                                                                                                                                                                                                                           /translation~"MTEAPKLKSGRARSGEAGSVRTLERGLSVLSALAELREATLTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLPPAEVRRKVGDGPFPAYTPHSITTLAALTRELNTVRGQDYALDDEERELGVRCLAT
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EELYVLKTTESGWENYLLDERFTTLPETHDRVWATFVTAKWEYAVESCDYDAVWERVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:X74409 SP:P42195 PID:396458 percent identity; 56.72; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to SP:P34798 PID:432629 percent identity: 57.45; identified by sequence similarity; putative"
                                                                                                                                           /note="similar to SP:P37728 GB:X62072 PID:49982 percent identity: 58.17; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:AL009126 percent identity: 58.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVRAASGEVVASLSVSAPTSRFPKKNIPDMLGRVQAASEQISARLGWRG"
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/protein_id="AAF10732.1"
/db_xref="GI:6458898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identified by sequence similarity; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conserved hypothetical protein"
/protein_id="AAF10731.1"
/db_xref="G1:6458897"
                                                                                                                                                                                                                                                                                                                        /product="transcriptional regulator"
/protein_id="AAF10730.1"
/db_xref="G1:6458896"
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/db_xref="G1:6458899"
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/gene="DR1159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5161. .6392)
/gene="DR1157"
                              complement(4153. .4956)
/gene="DR1156"
                                                                                           complement(4153. .4956)
/gene="DR1156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7360. .7905)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="DR1158"
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/gene="DR1160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="DR1159"
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      QRLHLSSDSEKPE"
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6657, ,722
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/translation="MNETQAAQLTRQVIDTCDALACHTEVPGEITRTYLCPTTRQVHE
ELRAMADRICHATVDAXGNIRSRIESRAPGARTLY IGSHLDTVPNARARYDGIIGVF
GYALVBALREBELPRYDAXGNISSRIESERYGARTLY IGSHLDTVBNARARYDGIIGVYF
ROAIVGYGLNPDELPGAGAEDRPLCYLEIH FBQGPVLUDQGAAVGVSAIVQSRLTL
HFTGRASHAGTTPMHIKRDALAAAARFIVGAEDLANKTPGIVATVGNIEARRGAVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAVQRALLFAQDTGAALHLVHVSSGAAVALAYEGKQKGIDVTIETCPHYLHFTGEDVE
RVGAALKCAPPLRDPAVQEELWRELLAGHIDTVGSDHSPAPPDWKTSEDFFSLWGGIS
GAGSTLNVMLEDGYAQRELLEIIBAALLALNPAQRFGLPQKGRLAVGADADFALVALG
EKFTLDTLYDRWQQNPYRGGSFQGRVHATYLRGQPVYQNGEFTGTPRGRLRPRSL"
complement(1451. .2701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MSLDLLLRGAVLVTPEGERRADLGIVGGQIAELTDEIATPAAQT
LDVSGLHVFPGVLDDHVHLNEPGRTHWEGFFTGTQALAAGGATSFLDMPLNSSPPVLT
RERFEDKARLGEEKSLIDFGLMGGLTPLNLDQLDDLAECGVIGLKAFMSHSGLDEFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P37113 GB:S67784 GB:X74289 PID:460895 SP:Q53389 percent identity: 55.20; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGEVSCSLDIRHADDAVRAQSLQELLALAEREAAARQVACSVTPRMAEAAVPMARSIR
ALLHQAREGGGITHPELVSGAGHDAQIMAQKWPAAMLFLRSPNALSHHPDEMAEPGDV
AAGIRVGTRFLELLAQAEQQVQA"
complement (1618 . 4089)
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ARAAATPDDEGRRABELLVERSDLDMHRRAVDSDAAVVDEDDTFSSTRDNVQASD
ALAWVAESDRPLLARTRALYALEPHLDFDGPAIAALCDLSAVLAARPERPIHTYVPKL
ETPARAQFWHDALLAEEHLSLAPNTVKTCLQIETFSGLLNIEAVFEPLAPRTYGLNA
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PRAPDRONGOPALGAVLADRÓREAAGGFRAAWAGLPELLEPWRRGFDAPAGSENKDTPA
PLAYHRLTDLPDPGPIRLADWREAAGGFRAAWAGCEGVLYAGRIEDTATAELARA
OLWGWVRVRAALEDGERLTPERYRQERRAVLGDDEPASRLLDHIVEAPACAATFPELEA
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Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Minton, K.W., Fleischmann, R.D., Ketchum, K.A., Nelson, K.E., Salzberg, S., Smith, H.O., Venter, J.C. and Fraser, C.M.
Direct Submission
Submitted (08-Nov-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /notes "similar to GB:U00096 SP:P77671 PID:1773192 PID:177852 percent identity: 64.13; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="N-carbamyl-L-amino acid amidohydrolase"
/protein_id="AAF10728.1"
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/protein_id="AAF10729.1"
/db_xref="G1:6458895"
                                                                                                                                                                                                                                                                                          /organism="Deinococcus radiodurans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="allantoinase, putative"
/protein_id="AAF10727.1"
/db_xref="G1:6458893"
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/gene="DR1154"
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complement(2698, .4089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(108. ,1454)
/gene="DR1153"
                                                                                                                                                                                                                                                                                                                                                                                                                       complement(108. .1454)
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                                                                                                                                                                                                                                              /translation~"MSGHPGLTTHVLDTARGKPAAGVRVQLCRVTGDTRTPVTEAVTN
SDGKTDAPLIERGSLKQGTYELTFHVADYFKGFVAAADPPFLDVVTLRFTVGDTSGHY
HVPLVMTPWSYSTYRGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Lranslation="MTREPVRMTRQGKERLEBQLQYLKTTRREQISEYMGKAIEDGDL
RESAAYDEARWQQSENEAKIAEIEAQLERAQIMKDEEIDTSAVGVGARVIVEDAQNKQ
RTLEIVGSFEVDVLKGKISDASPMGQALLGKRPGESAVWPGPKGNVSLKVISVEYP"
                                                                                                                                                                                                                                                                                                                                                                                                                               PID:606119 percent identity: 62.03; identified by sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P21346 GB:U01376 GB:X54718 PID:41611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 125020) Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hvang,H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10571 CCGGCAGTGGCAAGACCACCACGTGGCCAGCCTCATCGACTACCTCAACCGGCACTTCG 10512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10511 CCTATCACATTCTGACCATCGAAGACCCCATCGAGGTGCTGCACCGCAACAACCGCAGTC 10452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10391 CGCTGCGTCAAGACCCCGACGTGATCGTGATCGCCGAGATTCGGGAACCGCTGG 10332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10331 AGGCCGCGTGCTGCGGGGGCGCAGACCGGCATCTGGTCAGCACCCTGCACACCCAGG 10272
                                                                                     /note="similar to GB:AL009126 percent identity: 63.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 TTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 AACACCACAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 TATCCTCCTCCTGCTGCAGAAGAGAGATTGTCCACTGATCCGCATCTTCATCCACTCCTGG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 CTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 CCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCAGCCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 12334;
                                                                                                             identified by sequence similarity; putative"
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="transcription elongation factor"
/protein_id="AAF10735.1"
                                                                                                                                                                       /product="conserved hypothetical protein" /protein_id="AAF10734.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 46.2%; Pred. No. 1.6;
Matches 141; Conservative 0; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%; Score 42.6;
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                                                                                                                                                                                                                                                                                                                  complement(9370. .9846)
/gene="DR1162"
                                                                                                                                                                                                                                                                                                                                                      complement(9370. .9846)
/gene="DR1162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity; putative"
                                                                                                                                                                                                                          /db_xref="GI:6458900"
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                                                                                                                                                         /transl_table=11
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/gene="DR1161"
8900. 9750
                                                            /gene="DR1161"
                                                                                                                                     /codon_start=1
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/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
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NGAKYEGTWSNGLQDGYGTETYSDG"
32731 c 30696 g 28283 t 4254 others
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                                                                                                                                                                                                                                                    2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
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                            Stevanin, G., Brice, A.,
Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margolls, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
NAt. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                   Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="isolated from a patient with Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 41; DB 9; Length 125020; 11.4%; Pred. No. 5.3;
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/protein_id-"AAL40941.1"
/db_xref-"GI:17646245"
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/db_xref="taxon:9606"
/chromosome="16"
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1. .125020
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Matches 64; Conserve
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C12N15/00,
                                                                                                                                                                                                                                                                   PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
CIZNI5/09,CO7K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 TCAAAGCTGAACGGATGGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGGA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 PTGGCCTTGTGCAGGCCTGATGGCCACGTCTCTATGTCACCATCCGTCTGGGCATAA 412
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C12N5/10,C12Q1/68,
PC G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
PC G01N33/15,G01N33/50,G01N33/506,G01N33/574//A61K31/713,PC
                                                                                                                             17731 GKSKCWKRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCYSSMSCTSMYRCC 17790
                                                                     17671 MKGWRGSCWSSKWWGGSKSRSASSKCKGSRGMRRKSKKSSKYRKRGRGKKRSMTKSKGSK 17730
| 17611 GREMMMITYMCCCWRRRSYMYYRSMSAMGMRKSSWSGMRNMGSASSRRCKSASRSSWCSRR 17670
                                                                                                   842 TCCCAGTGGCTTGCCCCACCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACC 901
                                                                                                                                                                                                                                                                                                                                                                                               Kadota.M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
LUNX gene and method for detecting micrometastasis of cancer
Patent: JP 2001078772-A 1 27-MAR-2001;
OTSUKA PHARMACEUT CO LTD
                                          782 TGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCTGATTGGT 841
                                                                                                                                                                                                                                                                   LUNX gene and method for detecting micrometastasis of cancer. E53840
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JP 2001078772-A/1
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/ob_xref="taxon:32644"
217 c 204 g 190
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Matches 140; Conservative
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/Lranslation="MFQTGGLIVFYGLLAQTWAQFGGLPVPLDQTLPLNVNPALPLSP"
/Lranslation="MFQTGGLIJENLPLDILKPGGGTSGGLLGGLLGKYTSVIPGL
TCLAGSLTNALSNGLLGGCLGILENLPLLDILKPGGGTSGGLLGGLLGKYTSVIPGL
TNNIIDIXYPTOPQLLELGLVQSFDGHRLYYTPLGIKLQVNTPLVGASLLRLAVKLDIT
NNIIDIXYPTOPQLLELGLVQSFDGHRLYYTPLGIKLQVTPL
ARILAVBROKDETHLYLGDCTHSPGSLQISLLDGLGCPLPIQGLLDSLTGILNKVLPEL
VKGNVCPLVNEVLRGLDITLVNDIVNKLHGLQFVIKV"

285 c 258 g 243 t
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Submitted (28-JUL-1999) Molecular and Genetic Medicine, University
of Sheffield School of Medicine, Glossop Road, Sheffield S10 2RX,
UK
                                                                                                                                                                                                                                                                                                                                                         PRI 02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens Actacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Euveryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1011)
1 (bases 1 to 1011)
2 (bases 1 to 1011)
Characterisation of the human plunc gene, a gene product with an Characterisation of the human plunc gene, a gene product with an upper airways and nasopharyngeal restricted expression pattern upper airways and nasopharyngeal restricted expression pattern Blochim. Blophys. Acta 1493 (3), 363-367 (2000)
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                                                                                                                    533 GTGACTGCACCATTCCCCTGGAAGCTGCTAGTTGTTGTTGCTTGATGGACTTGGCCCC 592
                                                                                          563 GAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAA 622
                                          473 ACATCACTGCAGAAATCTTAGCTGTGAGAGATAAGCAGGAGGAGGATCCACCTGGTCCTTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="enriched in tracheal and nasal epithelium"
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503 TCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACCAGCCTGTTGCCGTCCTGG
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/db_xref="GI:7958616"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PLUNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF172993.1 GI:7958615
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Bingle, C.D.
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Matches 140; Conservative:
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    - 623 TCATCA 628 11 11 640 TCCCCA 645 . Σ δ

Bearch completed: August 6, 2002, 17:26:32 Tob time: 5124 sec

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BG870889

linear

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BG865861

BG869588 602789626 BG871442 602790649 BF535510 602050503

BG867259 602786288 BG870228 602793489

AA792682 vs75b09.r BG869519 602789531

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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
Insert Length: 472 Std Error: 0.00
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                  AI654622 384 bp mRNA linear EST 17-DEC-1999 wb48f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308941 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cyapbs-remail.uih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
_CDNA_Library_Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606" / /db_xref="taxon:9606" / /dbome="laMAGE:2308941" / /dbome="laMAGE:2308941" / /dbb="NOI_CGAP_GGG" / /tissue_type="pooled germ cell tumors" //db_bbst="Pooled germ cell tumors" //db_bbst="Pooled germ cell tumors" //db_bbst="py730-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism*"Homo sapiens"
                                                                         BG867408
BG872825
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BG865861
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BG866924
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AI654622
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AI654622/c
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                                                                                (without alignments)
8232.292 Million cell updates/sec
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BG865328 602783932
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AI218468 qh27e04.x
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                                                                                                                                       1 CACGAGATTTCATGAGCATC......aAGGCCCATTTCTGCAAAA 1028
                                                                       August 6, 2002, 14:03:33; Search time 1685.42 Seconds
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BG872461 6
         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                            13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                  - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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200.8
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Database

BG872403 602792704 BG865768 602784358 BG868020 602788382 BG869767 602789267

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from the normalized library NCI_CGAP_GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1228631, 1469064-1470983, and 1475592-147673). Subtraction by Bento Soares and M. Fatima Bonaldo.
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//lab_host="DH10B" -
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 472 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         850 GCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCACCTAACCAGC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   970 ACAGCAGCCTGTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAAAAA 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                           384 GTATCCTCCCTGCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 CICATITGAAGAGACGAAIGAGGAGGACCACIGIGGIGCAIGCIGAIIGGIICCCAGIG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGNAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCACAGTCAGA 969
                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                Score 341.4; DB 9; Length 384; Pred. No. 1.6e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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96.9%;
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FEATURES

TITLE

SOURCE

LOCUS

COMMENT

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Equal amounts of plasmid DNA from three normalized librariess (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR=amplified conns propols of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302097, 682632-687239, 1.M.A.G.E. 28711, and 729096-731399, Subtraction by Bento Soares and M. Felima Bonaldo.
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/lab_host="DH10B (Tl phage-resistant)"
/note="Corgan: salivary gland; Vector: pCMV-SPORT6; Site_l:
NotI: Site_2: Sali; Cloned unidirectionally. Frimer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG869528 891 bp mRNA linear EST 29-MAY-2001 602789545F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4921042 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIGSS row: i column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 803 GACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GACGAATGAGGAGGACCCCTGTGGTGCATGCTGATTGCTTCCCAGTGGCTTGCCCCACC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             863 CCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAG 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                  21.2%; Score 218; DB 9; Length 25 97.8%; Pred. No. 1.2e-47; ive 0; Mismatches 5; Indels
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/db_xref="taxon:10090"
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                                                                                                                                                                               40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC
Technologies. Note: this is a NCI_CGAP Library."
1 228 c 175 q 256 t
                                                                                                                                    0; Mismatches 347; Indels 41;
                                                                                             DB 10; Length 891;
                                                                                                Score 200.8; DB 10 Pred. No. 9.2e-43;
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/Clone_lib-"NCI_CGAP_SG2"
/Clone_lib-"NCI_CGAP_SG2"
/Clone_lib-"NCI_CGAP_SG2"
/Lab_host="D4HIOB (TIP phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_l:
NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
602791220F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922525 5'
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10842 row: g column: 06
High quality sequence stop: 893.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 896)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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/clone_lib="NCI_CGAP_SG2"
//lab_nost_DH0B (TI phage-resistant)"
//lab_nost_DH0B (TI phage-resistant)"
//note="Organ: salivary gland; Vector: pcMv-SPORT6; Site_l:
NotI; Site_2: Sali: Cloned unidirectionally, Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
1 214 c 172 g 246 t
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Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgupbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparalion: Life Technologies, Unc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10846 row: f column: 22
uich onality sequence stop: 835.
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602792983F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4924053 5',
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
520 ATTGAAACTGATCCCCAGACACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                            580 CCAACCAGCATCTCACTTTCTTGGTGGACAACACACAAATCATCAACAAAAAGGGGGG 639
                                                                                                                                                                                                       640 AATAGCCTGATCAACACCCTGAAAAGCACTGTATCTCCTCCTGCTGCAGAAGGAGATATGT 699
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                             183 ATTAAAACCAATCCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 542
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/db_xref="taxon:10090"
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BASE COUNT ORIGIN

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AK009032 972 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2300005806:parotid secretory protein, full insert
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  DB 10; Length 844;
  Score 198.4; DB 10; Length
Pred. No. 3.9e-42;
0; Mismatches 336; Indels
19.3%;
                                              Matches 471; Conservative
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                                                                                                                                                                                /organism="Mus musculus"
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/clone="230005806"
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                                                               Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2300005B06.
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK009032.1 GI:12843579
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/clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult"
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/translation="MFQLGSLVVLCGLLIGNSESLLGELGSAVNNLKILNPPSEAVPQ
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library, clone:2310075K06:parotid secretory protein, full insert
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                                                                                                                                                                                                                                                                                          700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                               669 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCTAAGTGTTCTTCAGGGTCTCCTCTT 728
                                                                                                                                                                                                                                                                                                                                                                                                 760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
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                                                                                                                                                                                640 AATAGCCTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Scalabor, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Bandarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Bulda, S., Fukunishi, Y., Furuno, M., Hanagak, T., Hara, A., Hayatsu, M., Hill, D., Hitamoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Nahi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, R., Saki, C., Sakai, K., Sano, H., Sasaki, D., Schin, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLINGELLOQATSWPLAKNSTLETLNTADLGRIKSFFSLNGLLKINNLKVLDFQAK
LSSNGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGK
CSSNTDKISISLLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10.70L-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, FIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehlro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, Pk. Intr., Yqenome-gsc.riken.go.jp, Tel:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome corrections of Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
The RIKEN Genome Exploration Research Group Phase II Team and the
                                                            Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 972)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 t
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/db_xref="taxon:10090"
/clone="2310075K06"
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/db_xref="GI:12845442"
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57. .764
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                                       FANTOM Consortium.
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57...7
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Gaps

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786 CACAACTCTCCTGCTGGCTACTCTCCCAGTGGTTTCATCTTACTTCTGATGGCATTTCCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549 ACAGATAAAATCTCCATTTCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCACCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      659 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGGTCTCTCTTCT 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 CCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAGCCTGAGTCCCCACCAGAAGGACCT 939
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                                                                                                             100 TCAGAGTCTCTTCTTCACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                 160 CCTGTTCTTCACGAGGGACTTGACACTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                   .-----AAATTCTGAATCCTCCTCTGAAGCTGTCCCTCAGAAC 191
                                                                                                                                                                                                                                                                                                                                            220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                              192 CTGAATCTGGATCTGGAGTTGGTTCAGCAAGCTAGCCACAAGTTGGCCATTAGCCAAGAACAGC 251
                                                                                                                                                                                                                                                                                                                                                                                                                              280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGGTGCTTCCAACTAACAGG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 ATTCTAGAAACGTFGAACACAGGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                    40 AGACAAAAGATGCTTCAGCTTTGCAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                             Indels 47;
    Length 972;
                                           0; Mismatches 360;
19.3%; Score 198; DB 11; 55.7%; Pred. No. 5.4e-42;
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RESULT

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/clone_lib-"NCI_CGAP_SG2"

/Lab_host="DH10B (TI phage-resistant)"
/hote="Organ: salivary gland; Vector: pcWV-SPORT6; Site_l:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                         EST 29-MAY-2001
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                            602792782F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923980 5'
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                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 ATTCTAGAAACGTTGAACACAGCGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 AATGGTTTATTGTTGAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 196.8; DB 10; Length 954;
Pred. No. 1.1e-41;
0; Mismatches 372; Indels 43; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTAGTCTTGTGGGCCTGCTCATTGGGAAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10846 row: c column: 21
High quality sequence stop: 823.
Location/Qualifiers
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                         linear
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                         mRNA
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/db_xref="taxon:10090"
/clone="IMAGE:4923980"
                         954 bp
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54.8%;
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                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                           mRNA sequence.
                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                     house mouse
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                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
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BG872461
                                                                                                                                   VERSION
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/db_xref="G1:12844581"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                            760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 CCAGGAAGCTGCTGCCACCACCTAACCAGGGTGAAAGCCTGAGTCCCACCAGGAGGACCT 939
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                                                                                                   520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                      474 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 533
                                                                                                                                                                                                           580 CCAACCAGCATCTCACTTTCCTTGCTGGACAACACAGCCAAATCATCATCAACAGTTCGTG 639
                                                                                                                                                                                                                                                           534 ACAGATAAAATCTCCATITCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 593
                                                                                                                                                                                                                                                                                                                    640 AATACCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                    594 GAIGGIGTCTCTACCCTCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTGCTAIGT 653
                                                                                                                                                                                                                                                                                                                                                                                                                          700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                714 AATCTACTG - GCAGGACAGGGTACAAATTGCCCTCTGAACGAGGAAGAACCGAAGGATG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      772 CACAATCTCCTGTTGGGTACTCTCCAGGGGGTATCATCTTACTTCTGATGGCATTTCCCT 831
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RirkB. integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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NLNLDVELLQQATSWPLAKNSILETLNTADLGNLKSFTSLNGLLLK1NNLKVLDFQAK
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                                                                                                                                                                                                                                                                                                                                                            Indels 47; Gaps
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/clone="IMAGE:4910430"
/clone="IMAGE:4910430"
/lab_host="ballog Tr] phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sali; Cloned unidirectionally. Primer: Oligo
AT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                           BG865328 892 bp mRNA linear EST 29-MAY-2001 602783932F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910430 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 892)
HT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgabbs-remail.nih.gov
Tissue Procurement: Joffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMIOSIO row: o column: 07
High quality sequence stop: 847.
                               880 CCAGGAAGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGGAATGTCGTGGATAAGCTGGAA 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------ 137
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0; Mismatches 347; Indels
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                                                                                                                         901 TCCCAAATTCTCTTCCTC 918
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Lo 870)

E 1 (bases 1 to 870)

NIH'MGC http://mgc.nci.nih.gov/.

NIH'MGC http://mgc.nci.nih.gov/.

L Onbublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: ggapbs:r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LiAM10820 row: 1 column: 02
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236 ATTCTAGAAACGTTGAACACGGGACCTTGGCAATTTAAAAAGGTTTACATCT----TTG 292
                                                                                                          293 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTGAGTGTT 352
                                                                                                                                                                                                                                                                                                                           520 ATTGAAACTGGTCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
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                                                                                 340 GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                      353 TCCAACGGCAATGGCAFTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 412
                                                                                                                                                                                                                                                                                               CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACACCAAATCATCAACAGTTCGTG 639
                                                                                                                                                                                    400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG
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Location/Qualifiers
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Source

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/clone="IMAGE:4914193"
/clone="lb="NCI_CGAP_SG2"
/lab_nost="D410B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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0; Mismatches 338; Indels
/organism-"Mus musculus"
                                                /db_xref="taxon:10090"
                       /strain="FVB/N"
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Matches 469; Conservative
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Location/Qualifiers
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/lab_host="DH10B (T1 phage resistant)"
/lab_host="DH10B (T1 phage resistant)"
/note="Norgan: allivary gland; Vector: pCMV-SPORT6; Site_l:
NotI: Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
1 248
                                                                                                                                                    BG870337 968 bp mRNA linear EST 29-MAY-2001 602791223Fl NCI_CGAP_SG2 Mus musculus CDNA clone IMAGE:4922669 5',
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                 NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 193.6; DB 10; Length 968;
53.6%; Pred. No. 8.1e-41;
Live 0; Mismatches 389; Indels 43; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLAM10842 row: m column: 06
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/clone="IMAGE:4922669"
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Matches 500; Conservative
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602792704F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4924056 5',
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                                                                           400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                               354 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 413
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/note="DHIOB (TI phage-resistant)"
/note="Organ: salivary gland; Vector: pcMv-SPORT6; Site_l: NotI: Site_2: Sali; Cloned unidirectionally, Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
/Technologies. Note: this is a NCI_CGAP Library."
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/clone_lib="NCI_CGAP_SG2"
/lab_host="DHIOB (T1 phage-resistant)"
/note="Corgan: salivary gland; Vector: pCMV-SPORT6; Site_l:
/nots: Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

268 c 205 g 294 t lothers
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Mammalia: Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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602784358Fl NC1_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910534 5
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phate: LLAM10811 row: c column: 15
High quality sequence stop: 832.
Location/Qualifiers
770 CACAACTCTTCTGGCTGGTTAATCTCCAGGGTTTCACCTTACTTCTGATGGCATTCCTT 829
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/clone="IMAGE:4910534"
                                                                    880 CCAGGAAGCTGCTGCCACCTAAC 905
                                                                                                                                        830 CTACAAAGTGGCAACTTTCATCACAC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="FVB/N"
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les 505; Conservative
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BG865768
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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602788382F1 NC1_CGAP_SG2 Mus musculus cDNA clone JMACE:4919756 5
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340 GACATITITGGGTTGAAAATCAGCAACTCCCTCATCCTGGAIGTCAAAGCTGAACCGATC 399
                                                             286 AATGGTTTATTGTTGAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGGTGTCT 345
                                                                                                                                                                                              405
                                                                                                                                                                                                                                                        460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                466 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACC 938
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 TCTTAGAAAGTIGT-ACTTATCATCCCACATTTCTACCTGAGACCAACCCAAAGGAGC 882
                                                                                                                              400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGGGAATGTCACTGTGGCCGGG
                                                                                                                                                                TCCAACGCCAATGCATTGATCTGACGGTGCCCTTGGCTGGGAAGCCTCCTTGGTTCTG
                                                                                                                                                                                                                                                                                          580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG
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Plate: LLAM10835 row: c column: 21
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 844.
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                                                                                                                                                                                                                                                                                                                                                               Query Match 18.6%; Score 190.8; DB 10; Length 889; Best Local Similarity 55.7%; Pred. No. 4.3e-40; Matches 428; Conservative 0; Mismatches 332; Indels 8;
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Search completed: August 6, 2002, 16:52:39 Job time: 10146 sec

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August 6, 2002, 16:18:33 ; Search time 208.17 Seconds (without alignments) 8478.590 Million cell updates/sec
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2. S1DS1/99gatu-yerreseq, emb1/Nk1990_DAT:*
3. S1DS1/99gatu-yerreseq/geneseqn emb1/Nk1990_DAT:*
3. S1DS1/99gatu-yerreseq/yercseqn emb1/Nk1991_DAT:*
4. S1DS1/99gatu-yerreseq/yercseqn emb1/Nk1993_DAT:*
5. S1DS1/99gatu-yerreseq/yercseqn emb1/Nk1994_DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn.embl/Na1984.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn.embl/Na1986.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/Na1986.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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1028
                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	************	Human parotid secr	Human secreted pro	CDNA encoding huma	Human protein enco	Human PRO1025 nucl	Human parotid secr	Expressed sequence	Expressed sequence	Expressed sequence
SUMMARIES			ID		AAV44759	AAA87727	AAF64009	AAH99686	AAC58379	AAV37699	AAV44760	AAV44761	AAV44762
			DB	1	19	21	22	22	21	19	19	19	19
			ore Match Length DB I		1028	1058	1058	1041	1049	824	449	538	359
	фP	Query	Match		100.0	99.2	99.5	96.7	96.3	79.6	37.3	36.5	30.4
			Score	,	1028	1019.8	1019.8	994.4	990.4	818.4	383.8	374.8	312.8
		Result	N		Н	73	m	4	2	<b>9</b>	7	80	σ

96US-0034429. 97WO-US23522.

18-DEC-1997; 23-DEC-1996;

02-JUL-1998.

AAV4476	AAC23485 Human secr	AAV44764	AAV44765	AAA61274	AAK89798 Human digestiv	ABA60313 Human	AAK08593 Human	AAK34475 Human	AAI40197 Probe #8883	ABA72852 Human foeta	AAK21285 Human brain	AAK47441 Human bone	AA153276		AAV44767 Expres	AAK87987	AAV44768 Expressed	AAH27756	AAX00808 LS170	AAH27757 Human	AAZ61165	AAX00809 LS170	AAS46111 Human	AAX59356 Human	AAS59237 Human	ABA90906 Human	AAI58877 Human	AAI60663 Human	AAK87982 Human	AAK87985 Human	AAI59757 Human polynucl	AAI57971 Human	AAD05509 Human secrete	AAV43243 MSRV-1 clone 8	AAH68310 C glutamicum CC	CHINDRICATIV
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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human; Human parotid secretory protein coding sequence. Location/Qualifiers 49..798 AAV44759 standard; DNA; 1028 BP. /\*tag= a /product= hPSP 49..102 /\*tag= b 103..795 16-OCT-1998 (first entry) therapy; diagnosis; ss. /\*tag= Homo sapiens. WO9828420-A1 sig\_peptide mat\_peptide AAV44759; 4AV44759 ACCONTRACTOR ACCON

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those characterised by overexpression and/or activation of the amplified antibodies and other compounds include benign or malignant tumours (e.g., remal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukäemias and lymphoid malignancies, other disorders such as neuronal, glilal, astrocytal, lypothalamic and other glandlar, macrophagal, epithelial, stromal and blastoceelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC5836 represent pcR primers and hybridisation probes used in the isolation of the human pRO sequences. AAC58367 to AAC58367 to AAC58367 to AAC58367 and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                        present invention.
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Sequence 1049 BP; 279 A; 299 C; 236 G; 235 T; 0 other;

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                                                                                85 GTGCTCACTGGGACCTCAGAGTCTCTTCACAATCTTGGCAATGACCTAAGCAATGTC 144
                                                                                                                                                   145 GIGGATAAGCIGGAACCIGITCTICACGAGGACTIGAGACAGTIGACAATACTCTTAAA 204
                                                                                                                                                                                                                   223 ggcatccttgagaaactgaaggtcgacctaggagtgcttcagaaatccagtgcttggcaa 282
                                                                                                                                                                                                                                                                                                                                                    205 GGCATCCTTGAGAAGCTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AAAGCTCAACCGATCGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAAT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 aaagctgaaccgalcgatgatggcaaaggccttaacctgagcttccctgtcaccgcgaat 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 CTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 GAATGUGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATC 624
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                                   0; Gaps
                                                                25 TCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGCAAACTTGTTCTCCTGTGCGGC 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%; Score 990.4; DB 21; Length 1049; 99.4%; Pred. No. 6.3e-290;
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that bind specifically to, and modulate activity of HBSP are used to treat cancer and autolmmune diseases particularly of secretory or treat cancer and autolmmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, or caves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HBSP nucleic acid are used to produce recombinant HBSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HBSP-expressing cells, to detect cells
                                                                                                                                                                    Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal tissue; HPSP; Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA encodes a human parotid secretory protein (HPSP). Antagonists
805 CGAATGAGGAGCACCACTGTGGTGCTATTGGTTCCCAGTGCCTTGCCCCACCCCC 864
                                    823 cgaatgaggaggaccactgtggtgcatgctgattggttcccagtggcttgccccacccc 882
                                                                         865 TTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTC 924
                                                                                                             883 ttatagcatctccctccaggaagctgccaccacctaaccagcgtgaaagcctgagtc 942
                                                                                                                                                  925 CCACCAGAAGGACCTICCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACA 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                  /product= "parotid secretory protein"
/note= "#"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human parotid secretory protein (HPSP) encoding DNA.
                                                                                                                                                                                                                                                                 1003 catgttgtcctgccctggcaataaaggcccatttctgca 1042
                                                                                                                                                                                                                           985 CATGTTCTGCCCTGGCAATAAAGGCCCATTTCTGCA 1024
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             AAV37699 standard; DNA; 824 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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AAV44760 standard; DNA; 449 BP

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that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 CANTGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ACTIGITCICCIGICGGCGTGCTCACIGGGACCICAGAGTCITCTIGACAAICTIGG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 824 BP; 226 A; 225 C; 184 G; 189 T; 0 other;
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                                                                                               by hybridisation, particularly con-
but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                          Best Local Similarity 99.9
Matches 819; Conservative
                                                                                                                                                                                                                                                     Query Match
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RESULT AAV44760

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DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The HPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in stendard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the sallvary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antibacterial, antibacterial, antipacterial, or calls expressing it, are used in screening tests to
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                                                                                                                                                              Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CACGAGATITCAIGAGCAICCICCICIAAACGCGIGICAAGACAAAAGAIGCIICAGCII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an expressed sequence tag with homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to identify hPSP-binding proteins.
                                                                                                                         Expressed sequence tay HSGSA61R.
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                                                                               16-OCT-1998 (first entry)
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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention encodes the human parotid secretary protein (hBSP). The hBSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hBSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hFSP. The protein is also useful as antifungal, antibacterial, antibacterial antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (antipagnists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                      AGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGA 293
                                                                                                                          243 aggagtgetteaywaateeagtgettygeaaetggeeaageaggeecaaggaagetga 302
                                                                                                                                                                  294 GAAATTGCTGAA-CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGT 352
                                                                                                                                                                                                             gaaattgetgaaccaatgleattletaagetgetteeaaettaacaeggaeatttttgggg 362
                                                                                                                                                                                                                                                    TG-AAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATGATGATGGCAAA 411
                                                                                                                                                                                                                                                                                            363 igaaaaaicagcaacieceicaicelgaigaigaigaageigaaecegaicgaigaigaagaaa 422
181 GAGACAGTTGACAATACTCTTAAAGG·····-CATCCTTGAGAAACTGAAGGTCGACT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                       412 GGCCTTAACCTGAGCTTCCCTGTCACC 438
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the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
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                                                                                                                                                                                                                                                                              71 TTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGGCAATG 130
                                                                                                                                                                                                                                                                                                                                                     131 ACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGTTG 190
                                                                                                                                                                                                                                                                                                                                                                      191 ACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAAAT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                             251 CCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAAAAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 TCATITCIAAGCTGCTICCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAACTCCC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 tecetgiteacegggaatgiteaanginggeeegggeeenteatigggeeagnitateaa 479
                                                                                                                                                                                                                                                                                                               61 ttctcctgtgcggcgtgctcactgggacctcagagtctcttcttgacaatcttggcaatg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ccagigotiggcaaciggcoaa cagaaggnocaggaagcigagaatigcigaacaaig 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 TCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACC----TGAGC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ncanccggatgttcaaagntgnancgatcgatgatgggcaaaggctttaanccggaggct 419
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                                                                                                                            36.5%; Score 374.8; DB 19; Length 538;
87.7%; Pred. No. 2.5e-103;
.ive 0; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                       12 ATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCT-TCAGCTTTGGAAACTTG 70
                                                                                                                                                                                                                                        1 atyagnatectectetaaaegegtyteaagacaaaagatgetnneagetttggaaaettg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 -- CCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCC 535
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Best Local Similarity 87.7%
Matches 469; Conservative
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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention of contained within the DNA of the invention. The DNA of the invention of the invention of concess the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, of hPSP. The protein is also useful as antifungal, antibacterial, DNA. The protein or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antibitions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to example the antibition and this can be used to example the protein and this can be used to express the recombinant protein and this can be used to express the recombinant protein and this can be used to express the recombinant protein and this can be used to express the recombinant protein and protein and the protein and protein and the protein and                                                                                                                                                                                                   New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
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                                                                                                                   WPI; 1998-377651/32.
                                            Duan R, Ruben SM;
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Score 312.8; DB 19; Length 359; Pred. No. 1.3e-84; 0; Mismatches 7; Indels 3; Sequence 359 BP; 94 A; 79 C; 90 G; 90 T; 6 other; Query Match 30.4%; Best Local Similarity 97.2%;

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3; .Gaps

0; Mismatches

Matches 347; Conservative

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61 TGGAAACTTGTTCTCCTGTGCGGGGTGCTCACTGGGACCTCAGAGTCTCTTGACAAT 120
                                                                                                                          121 CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCT-GGAACCTGTTCTTCACGAGGGACT 179
                                                                                                                                                                                                                                                                                                                                          183 tgagacagttgacaatactcttaaagycatccttgagaaactgaaggtcganctaggagt 242
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                                                                                                                                                                                                                                                                                           180 TGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGT 239
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                                                    3 cacgagatttcatgagcatcctcctctaaacgcgtytcaagacaaaagatgcttcagctt 62
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Expressed sequence tag HSPAI14R.
                AAV44763 standard; DNA; 374 BP
                                                16-OCT-1998 (first entry)
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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention and is all so specifically stated as not being encodes the human parotid secretory protein (IPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding penomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, and antiparastic and analysis and may be expressed in vivo from the
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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
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                                              therapy; diagnosis; ss.
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644 GCGTGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCAC 703 704 TGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 763 74 tgatccgcatcttcatccactccctggatgtgaatgtcattcagcaggtcgtcgataatc 133 764 CICAGCACAAAACCCAGCIGCAAACCCICATIIGAAGAGGACGAAIGAGGAGGACCACIG 823 134 ctcagcacaaaacccagctgcaaaccctcatctgaagaggacgaatgaggaggaccactg 193 194 tggtgcatgctgattggttcccagtggcttgccccaccccttatagcatctccctag 253 GAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCT-GAGTCCCACCAGAAGGACCTTCC 942 4; Gaps 29.5%; Score 303.6; DB 19; Length 374; 95.0%; Pred. No. 8.3e-82; 14; Indels 0; Mismatches Matches 343; Conservative Local Similarity Query Match

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737 ATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTT 796

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menas encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different Lissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oliqo-dT primed cDNA libraries. Such ESTS are not well suited for isolating CDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and even in those cases where longer used to obtain full length cDNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures -
943 CAGATACCCC-TTCTCCTCACAGTCAGAACAGCAG--CCTCTACACATGTTGTCCTGCCC 999
                                        present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 317 BP; 82 A; 100 C; 68 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 27560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 27560; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC23485 standard; cDNA; 317 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0122487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
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                                                                                                                                                                   1000 C 1000
                                                                                                                                                                                                                                                     374 c 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC23485;
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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;

therapy; diagnosis; ss.

WO9828420-A1. Homo sapiens.

(HUMA-) HUMAN GENOME SCI INC.

96US-0034429. 97WO-US23522.

18-DEC-1997; 23-DEC-1996;

02-JUL-1998.

Expressed sequence tag HSGSC78R.

16-OCT-1998 (first entry)

AAV44764;

AAV44764 standard; DNA; 406 BP.

RESULT 12 AAV44764

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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention of the invention of contained within the DNA of the invention. The DNA of the invention of the corresponding encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding openomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening teach identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisonse nucleic acids, which are potentially useful for treating antisonse nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
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617 GCCAAATCATCAACAAGTTGGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCT 676

29.4%; Score 302.4; DB 21; Length 317; 99.7%; Pred. No. 1.8e-81; tive 0; Mismatches 1; Indels 0;

Conservative

Similarity

Best Local Sim. Matches 303;

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1 gocaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaagcactgtatcct 60

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                                                                                                                                                                                                                                       120 tgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagacagt 179
                                                                                                                                                                                                                                                                                                                                                                      189 TGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                             249 ATCCAGTGCTTGCCAACTGGCCAAGCAGAAGGCCC---AGGAAGCTGAGAAATTGCTG-- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 atccagtgcttggcaactgggccancagaaaggcccagggaaagcggagaaattgctgga 299
                                                                                                                                                                                                                     69 IGTICTCCTGTGCGGGGGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGGCAA 128
                                                                                                                                                                                                                                                                                             129 TGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGT 188
                                                                                                                                                                                                                                                                                                                                                                                                        180 igacaatacicitaaaagycatccitgagaaacigaaaggicgacciaggagigcitcagaa 239
                                                                                                                                              9 TTCATGAGCATCCTCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an expressed sequence tag with homology to to DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The HPSP DNA is
                                                                                                        B; Gaps
                                                                                                                                                                                  1 ttcatgagcatcctcctcttaaacgcgtgtcaagacaaaagatgcttca-ctttggaaact 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive
                                                                                                                                                                                                                                                                                                                   DB 19; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 -- AACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGG 351
                                                                                                          Indels
               Sequence 406 BP; 110 A; 95 C; 95 G; 100 T; 6 other;
                                                                   25.2%; Score 258.8; DB 1'89.4%; Pred. No. 3.4e-68; iive 0; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and endocrine disorders and for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tag HSPMD56R.
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                                                                                       Best Local Similarity 89.4 Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
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useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                                                                                                                                                                                    DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 TGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 tgttttccagacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctga 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 AAAGCACTGTATCCTCCCTGCTGCAGGAGGAGATATGTCCACTGATCCGCATCTTCATCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 aaagcactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatcc 202
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Birse CE, Carter KC, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identify hPSP-binding proteins.
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26-JUL-2000;
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16-MAR-2000;
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25-SEP-2000;
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22-AUG-2000;
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30-AUG-2000;
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                                                                                                                                                                                                                                                             The present sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number and the clone it was derived from are given in the descriptor line.

The invention relates to 31 novel genes and their fragments (nucleic acid sequences: AAA61260-A6129); amino acid sequences AAB12301-B12371) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides, in a sample or by determining the presence of mutations in the new polymolecides. Specific uses are described for each of the 31 polymucleotides, based on which tissues they are most highly expressed in and include products for the diagnosis or treatment of cancer, tumours, AIDS, autoimmune disorders, allergy, cardiovascular disorders, tumours, and include products for the genes are used to generate fusion proteins by linking to the gene a human immunoglobulin portion (AAA61251) for increasing stability of the fused protein as compared to the
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Best Local Similarity 95.2%; Pred. No. 1.6e-47;
Matches 197; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                       Novel human secreted proteins useful for diagnosing, preventing, treating and ameliorating a medical condition e.g. cardiovascular
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                              WPI; 2000-387729/33.
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2000US-0237037

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Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.

Disclosure; SEQ 1D NO 3374; 986pp; English.

Search completed: August 6, 2002, 17:28:16 Job time: 4183 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	equence 1	9 6	equence 379	equence 494	equence 226	equence 285	521,	982	3,	33384,	equence 2, Ap	2764,	2204,	2204,		5582,	5582,	æ	46041,	46041,	1950,	2930, A	1741, A	95211,	95211,	95211,	0	97422,	97422,	C
DI	S-08-993-529-1	-09-469-099-26 -09-599-360B-2	-09-758-472-	9-652-122-49	-09-726-170-22	5-09-726-175-28	-US00-35017A-5	-09-471-275-30	-10-081-056-16	0-324-185-33	-08-749-288-	-09-652-122-27	-60-250-830-22	-60-323-966-22	9-726-17	-09-834-366-55	-60-197-873-55	-09-758-472-17	-09-834-366-46	-60-197-873-46	-09-726-170-19	-09-652-122-29	-09-726-170-17	-09-528-409-95	-09-933-524-95	-09-933-524A-952	-09-528-409-97	-09-933-524-9742	-09-933-524A-974	-652-122-274
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                                                                   TGGAAACTIGTTCTCCTGTGCGGCGTGCTCGTGGGACCTCAGAGTCTCTTGACAAT 120
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                                                                                                                                                                                                                                                                                     CTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGGACATTTTTGGGTTGAAATC 360
                                                                                                                                                                                                                                                                                                            CTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATC 480
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                   1 CACGAGATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTT
                                                                                                        121 CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTT
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  Sequence 4862, Ap
Sequence 1332, Ap
Sequence 10989, A
Sequence 96481, A
Sequence 96481, A
Sequence 96481, A
Sequence 97559, A
Sequence 97559, A
                                                                                                                           Sequence 551, App
Sequence 3212, Ap
Sequence 10, Appl
Sequence 43461, A
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US-09-652-122-4862
US-09-23-972-10389
US-09-204-939-10389
US-09-904-93-10989
US-09-933-524-96481
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US-09-933-525-10
US-08-975-985-3212
US-08-975-985-3212
US-09-933-529-10
US-08-975-985-3212
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100.0%; Score 1028; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.3e-279;
Matches 1028; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 Sequence 1, Application US/08993529
GENERAL INFORMATION:
PAPLICANT: DUAN, ROXANE
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: Parotid Secretory Protein
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALICHARANCE ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTER STICS:
LENGTH: 1028 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) FEATURE:
    \frac{1}{2}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: sig_peptide
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LOCATION: 103..795
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STRANDEDNESS: single
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US-08-993-529-1
                                                                                                                                                                                                                                        RESULT 1
US-08-993-529-1
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 STATE:
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444 cttccctgtcaccgcgaatgtcactgtggccgggcccatcattggccagattatcaacct 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1996-12-22
PRIOR PEDITON NUMBER: 60/141,032
PRIOR PELLING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/113,686
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LOCATION: 67..111
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                                                                                                                                         APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.050AUS
CURRENT APPLICATION NUMBER: US/09/469,099
CURRENT FILING DATE: 1999-12-21
EARLIER FILING DATE: 1998-12-22
EARLIER FILING DATE: 1998-12-22
EARLIER FILING DATE: 1998-12-22
EARLIER FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PATENTY
EARLIER FILING DATE: 1999-06-25
SOFTWARE: DATE: 1999-06-25
EARLIER FILING DATE: 1999-06-25
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OTHER INFORMATION: seq QLWKLVLLCGVLT/GT
FEATURE:
NAME/KEY: polyA_Signal
LOCATION: 1023..1028
FEATURE:
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OTHER INFORMATION: Von Heijne matrix
                                           Sequence 26, Application US/09469099 GENERAL INFORMATION:
                                                                                             APPLICANT: Dumas Milne Edwards, J. APPLICANT: Duclert, A.
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Best Local Similarity 99.8
Matches 1021; Conservative
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; LOCATION: 1042..1058
US-09-469-099-26
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FEATURE:
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                            US-09-469-099-26
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Bougueleret, L.
APPLICANT: JODERT, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides FILE REPERENCE: GENSET.050CP3
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ORGANISM: Homo sapiens
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                                                                                                                                                                                   0; Mismatches
OTHER INFORMATION: seq QLWKLVLLCGVLT/GT
                                                                                                                                                                                   Conservative
               NAME/KEY: polyA_signal LOCATION: 1023..1028
                                                 ) NAME/KEY: polyA_site
) LOCATION: 1042..1058
US-09-599-360B-26
                                                                                                                                                                 Similarity
                                                                                                                                                                                 Matches 1021;
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DB 29; Length 1057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PHOOI CURRENT APPLICATION NUMBER: US/09/758,472 CURRENT APPLICATION NUMBER: US/09/758,472 CURRENT FILING DATE: 2001-01-11 PRIOR PLICATION NUMBER: 60/179,065 PRIOR FILING DATE: 2000-01-31 PRIOR FILING DATE: 2000-02-04 NUMBER: 05.000-02-04 NUMBER OF SEQ ID NOS: 9632
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3794, Application US/09758472; GENERAL INFORMATION:
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549 IGTIGCCGICCTGGGAGAAIGCGCCAGIGACCCAACCAGCAICTCACTITCCTIGCIGGA 608
                                       552 tgttgccgtcctgggagaatgcgccagtgacccaaccagcatctcactttccttgctgga 611
                                                                            609 CAAACACGCCAAATCATCAACAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCAC 668
                                                                                              669 TGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCT 728
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREPOR
FILE REFERENCE: 1600.1194-001
CURRENT APPLICATION NUMBER: US/09/652,122
CURRENT APPLICATION NUMBER: 60/151,421
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
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SOFTWARE: FastSEQ for Windows Version 4.0
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; GENERAL INFORMATION:
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APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFORD TITLE OF INVENTION: THE OFFICE OF
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                                                                              ; ORGANISM: Homo sapiens US-09-726-170-2263
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Matches 1020; Conserv
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APPLICANT: Fraser, Christopher C.
APPLICANT: Donovan, Michael J.
APPLICANT: Holtzman Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2054-001
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CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,859
PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                     Sequence 2853, Application US/09726175 GENERAL INFORMATION:
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                                                                                                                               GGACAAACACACCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG
                                                                                                                                                                                                          CACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTC
                                                                                                                                                                                                                                                                                                                                                          786 AACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCTGCTGATTGGTTCCC
                                                                                                                                                                                                                                                                                                     938 cagogigaaagcotgagtcccaccagaaggacottcccagataccccttctcctcacagt
96.7%; Score 994.4; DB 1; Length 1041; 98.8%; Pred. No. 4.3e-270;
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GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US00/35017A CURRENT FILING DATE: 2000/112-22 PRIOR PPLICATION NUMBER: US09/488,725 PROR FILING DATE: 2000-01-21 PRIOR APPLICATION NUMBER: US09/552,317 PRIOR FILING DATE: 2000-04-25 NUMBER: OF SEQ ID NOS: 1478
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Matches 1012; Conservative
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PCT-US00-35017A-521
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                                                                                               186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA
                                                                                                                                                                                                                          GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAA
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TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782
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1025 AAAA 1028
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: LOCATION: (53)...(40)

: OTHER INFORMATION: similar to gil710367 in the genepept database release 114,

: OTHER INFORMATION: Kun with FASTXY 3.3t00, default parameters

US-09-471-275-3095
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CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-10-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER APPLICATION NUMBER: US 09/277,490
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER APPLICATION NUMBER: US 09/309,720
EARLIER APPLICATION NUMBER: US 09/309,720
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
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ORGANISM: Homo sapiens
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426 CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGCCCATCATTGGCCAGATTATCAAC-C 484
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                                                                                                                                                                                                                                                               485 TGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACAC
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                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P3235PICI
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephan, Jean-Philippe F. Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 163, Application US/10081056 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen, Mary E. Goddard, Audrey E. Godowski, Paul J. Gurney, Austin L. Hillan, Kenneth J.
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
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Paoni, Nicholas F
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```